10-524 FOR OFFICIAL USE ONLY

204414

Scientific and Technical Information Center

SEARCH REQUEST FORM
Requester's Full Name: TANE ZALA Examiner #: 77512 Date: 10-12 Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10604721 Location (Bldg/Room#): 8000 Mailbox #): 2018 Results Format Preferred (circle): PAPED DIS ***********************************
To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:
Title of Invention: Bio IN FORMATICALLY DETECTABLE,
Inventors (please provide full names): Bentuich
Earliest Priority Date: 8-13-63
Search Topic: Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter, elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept of Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.
For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent number, appropriate serial number.
Please Search Seg ID No: 8797 Please limit to 120 NTS.
Plene Send Seg ID Nov.: 5135, 6033, 5136 + 60:
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AR238589 Sequence
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AR628705

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/mol_type="unassigned DNA"
/db_xref=xxxon:32630"
/note="Computer Generated Probe Sequence."
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Patent: WO 0215649:-A 365 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
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Sequence 4341 from Patent WO0216649.
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AX447886.1 GI:21696785
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AX004269
AR139887
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AR100388
AR150043
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AR442443
AB213914
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synthetic construct
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AUTHORS
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AX447886
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162320 Sequence 23
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AX215299 Sequence
AX215300 Sequence
AX298773 Sequence
AX347840 Sequence
AX65252 Sequence
CS101953 Sequence
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BD141786 Novel G p
BD173668 Novel phy
BD181737 Novel G p
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AX538707 Sequence
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                    GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                                                     6366136 seqs, 31973710525 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - nucleic search, using sw model
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BD1417868
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AX447886
AX538707
AR036420
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Gapop 10.0 , Gapext 1.0
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90 - pat.; 

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Match
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Database :

PAT 03-JUL-2002

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Gaps

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115.8 113.8 113.8 113.4 113.4 113.2

Result

12.8 12.8

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PAT 03-JUL-2002

synthetic construct synthetic construct

(CEMI -) CEMINES INC WPI; 2006-047578/05. Neuman T; products.

Detecting open chromatin comprises determining hybridization of the capture probe to the treated- and untreated-sample amplification

Example 1; Page 37; 43pp; English

de de bubblication teacturion using a second amplification reaction using a second amplification reaction using a second portion of the chromatin sample, where the second portion is not treated with the open chromatin pade leaving agent, to produce untreated-sample amplification products and the untreated-sample amplification products and the untreated-sample amplification products probe; and determining the hybridization of the capture probe to the products, where probe, and where reduced hybridization of the capture probe to the capture probe to the untreated-sample amplification products secondaried to the hybridization of the capture probe to the capture probe to the untreated-sample amplification of the capture probe to the untreated-sample amplification products

I a chromatin in genomic DNA. The methods and chromatin state profiling array a determining the hybridization of a capture probe to a treated sample amplification products and the untreated sample amplification products. Specifically, the method comprises preparing a chromatin sample from cells, the chromatin sample comprising genomic DNA segments or genomic DNA with one or more open chromatin sites; treating a first portion of the chromatin sample with an open chromatin DNA cleaving agent to produce fragments; performing a first amplification reaction using the fragments as a substrate, to produce treated-sample amplification products; treatment and evaluating the response of cells and patients to candidate or established therapeutic agents. The present sequence is a 3' reverse open chromatin in genomic DNA by chromatin for monitoring or established therapeutic agents. The present sequence is a primer for one-sided PCR amplification of DNase I treated chr fragments, deposited on a chromatin profiling array diagnostic and prognostic methods, and are useful new invention relates to detecting

Sequence 25 BP; 13 A; 0 C; 11 G; 1 T; 0 U; 0 Other

ö Query Match 65.0%; Score 15.6; DB 15; Length 25; Best Local Similarity 40.9%; Pred. No. 4.5e+03; Matches 9; Conservative 9; Mismatches 4; Indels (

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Gaps

a 8

RESULT 10

BP. ADI94591/c ID ADI94591 standard; DNA; 21

(first entry) 04-NOV-2004

ADI94591;

Murine IFN-gamma associated probe SEQ ID 2144.

functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; ss; probe.

Mus musculus.

29-NOV-2001

WO200190337-A2

24-MAY-2001; 2001WO-US017086

1-JAN-2001;

2001US-00758282 2001US-00864426 2001US-00864636 24-MAY-2001; 24-MAY-2001;

(THIR-) THIRD WAVE TECHNOLOGIES INC.

Hall JG; V, Ma W; Takova TY; Chehak L, Curtis ML; Bis PS, ski RW, Lukowiak AA, Lyamichev Schaefer JJ, Skrzypczynski Z, Neri BP; Bartholomay CT, Chehak ser M, Kwiatkowski RW, Allawi H, Bartholomay CT, Ip HS, Kaiser M, Kwiatkow Olson-Munoz MC, Olson SM, Lyamichev NE, vedvik KL,

WPI; 2002-083110/11.

RNA Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNF target

Claim 95; SEQ ID NO 2144; 1266pp; English

This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered functionality in a nucleic acid cleavage assay. The enzyme comprises a 5' nuclease, preferably a thermostable 5' nuclease, or a polymerase so in collected to a naturally occurring sequence of a attered in sequence related to a naturally occurring sequence of a collected in sequence related to a naturally occurring sequence of a the naturally occurring polymerase. Preferably the polymerase is a thermostable polymerase from a Thermus species such as T. aquaticus, T. C. T. thermophilus, T. filiformus or T. soctoductus. The enzyme comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid comprises an entitle sequence that provides improved background specificity in the nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises of fluorescence energy transfer or by detecting fluorescence, mass or fluorescence energy transfer or by containing and acid acid involves exposing a sample (a cell lysate) comprising substrate cleavage product. The enzyme is useful for cleaving a nucleic acid conprising wild-type and mutant allease of genes including genes conduction the animal or plants that are or may be associated with the animal or plants that are or may be associated with the animal or plants that are or may be associated with

disease or other conditions. In addition, the enzymes may be useful for detecting and identifying strains of microorganisms including bacteria, fungi, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human immunodeficiency virus

Sequence 21 BP; 9 A; 3 C; 8 G; 1 T; 0 U; 0 Other;

Length 21, 3; Indels Score 15.2; DB 7; Pred. No. 6.6e+03; 7; Mismatches 3; 63.3%; Query Match
Best Local Similarity Surve

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Gaps

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GUCUCCUTUCGCCACCUC 24 20 GICTCTCTTTTGCCAGITC 1

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BP. ADI94589 Btandard; DNA; 22 04-NOV-2004 (first entry) ADI94589; RESULT 11 ADI94589,

Murine IFN-gamma associated probe SEQ ID 2142.

Oligonucleotide array; adapter sequence; probe; ss.

27-AUG-2001; 2001WO-US026519

WO200216649-A2

Synthetic.

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Gaps

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28-FEB-2002

2000US-0227948P 2000US-0228854P

25-AUG-2000; 29-AUG-2000;

(ILLU-) ILLUMINA INC

WPI; 2002-292068/33.

Gunderson K;

Oligonucleotide adapter/capture probe 12529.

11-JUN-2002

ABQ12538;

ABQ12538 standard; DNA; 25 BP

RESULT 12

ABQ12538

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nucleic acid sequence by attaching a adapter nucleic acid (AB000010-AB013409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (1). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                 / Match 18.6%; Score 15.8; DB 6; Length 24; Local Similarity 73.7%; Pred. No. 5.9e+04; He 14; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide array, adapter sequence, probe, ss.
                                                                                                              Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                       16 GAGAGGGCUGGUUAAGGC 34
                                                                                                                                                                                                                                              GAGAGGCGTTGGTTAAGGC 22
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ABQ11043/c
ID ABQ11043 standard; DNA; 24 BP.
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29-AUG-2000; 2000US-0228854P.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Array comprising adapter sequences useful for immobilizing or detecting target nucleic acid sequence, has different addresses comprising different specific capture probes.

Claim 1; Page 244; 261pp; English.

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The invention relates to an oligonucleotide array (I) comprising at least different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. [I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
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Pred. No. 6e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
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Best Local Similarity 73.7%;
Matches 14; Conservative
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ABQ12579 standard; DNA; 25
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Gaps

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18.6%; Score 15.8; DB 6; Length 24; 73.7%; Pred. No. 5.9e+04; ive 3; Mismatches 2; Indels

16 GAGAGGGCUGGUUAAGGC 34

ò

Local Similarity 73.7

Best Loca Matches

Query Match

||||||| | :||::||||| GAGAGGCGTTGGTTAAGGC 3

OM nucleic

Run on:

Sequence:

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PAT 02-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 06-AUG-2001
AR340859 Sequence
AR118827 Sequence
AR126073 Sequence
AR473711 Hepatitis
BR473711 BR41 Hepatitis
BR473711 BR473711 BR473711 BR478111 BR478111 BR478111 BR47811 BR4781 BR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCUUCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
assessment, prevention, and therapy of cervical cancer
Patent: WO 014267-A 193 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Sequence 193 from Patent WO0142467.
AX184498

    .97
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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CQ534358
MMTRB138
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CQ154107
CQ186687
CQ237346
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CQ311944
CQ319349
AX992911
RNU12526
AR166135
AR236505
AR279563
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                            Homo sapiens (human)
                                                                             Hominidae; Homo.
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SOURCE
ORGANISM
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VERSION
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TITLE
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AX184498
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AX772410
LOCUS
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AY753641 Sus scrof
AR165723 Sequence
AR304919 Sequence
BD034273 Sequence
AR734534 Sequence
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AX987628 Sequence
BD122487 EST and e
AR426934 Sequence
E08253 linker. 9/1
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E08252 linker. 9/1
AX184576 Sequence
BX294351 Arabidops
A86879 Sequence 19
BD070385 Factor X-
                                                                                      October 16, 2006, 14:22:20 ; Search time 1299 Seconds (without alignments) 3889.027 Million cell updates/sec
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              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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AR165723
AR304919
BD034273
AR334534
AX388740
EWU12530
E08252
AX184576
BX294351
BMC194351
BD070385
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Maximum Match 100%
Listing first 45 summaries
                                                              nucleic search, using sw model
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AX772410
AX987628
BD122487
AR426934
E08253
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Gapop 10.0 , Gapext 1.0
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79
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44
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Match Length DB
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gb_pat:,
gb_pl:.,
gb_pr:,,
gb_sy:,,
gb_un:,
gb_ov:,,
gb_ov:,,
gb_ni:,
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seq length: 100
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Perfect score:
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Minimum DB Maximum DB

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PAT 29-SEP-1997
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homonindae; Homo.

1 (bases 1 to 93)
Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
Est and encoded human protein
Patent: JP 2002010789-A 14564 15-JAN-2002;
                                                                                                            OS Homo sapiens (human)
PN JP 2002010789-A/14564
PD 15-JAN-2002
PF 07-AUG-1999 US 60/147499
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE GIORDANO
PC C12N15/09, C12N15/09, C12N15/09, C12N15/09, C12N15/09
                                                                                                                                                                                                                                                                                           C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,
C12N15/00
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Unclassified.
1 (Dases 1 to 93)
Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Parent: US 6619063-A 18431 28-OCT-2003;
Genset S.A.;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GGCGGGGAGACGAGCGGCUCUGGCCCCUUAAUU 40
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    .93
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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/organism="unknown"
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Matches
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AUTHORS
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JOURNAL
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TITLE
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KEYWORDS
SOURCE
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E08253/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                  Dickson, B., Berger, J., Suzuki, T. and Knoblich, J.
Method for identifying therapeutic targets by use of genetic screens in drosophila melanogaster
Patent: WO 03042407A 200 22-MAY-2003;
BOEHRINGE INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 49;
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                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                      ch 25.6%; Score 20.2; DB 2; 11 Similarity 51.5%; Pred. No. 2.3e+04; 17; Conservative 8; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESTs and encoded human proteins
Patent: EP 1104808-A 18431 06-JUN-2001;
Genset (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 bp DNA
Sequence 18431 from Patent BP1104808.
AX987628
AX987628.1 GI:40993768
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     Sequence 200 from Patent WO03042407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .93
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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EST and encoded human protein.
BD122487
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JP 2002010789-A/14564.
Homo sapiens (human)
Homo sapiens
                        AX772410
AX772410.1 GI:32438983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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Best Local Similarity
Matches 17; Conserva
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AX987628/c
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PAT 17-OCT-2001
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<1. .>92
/gene="CREB"
/gene="CREB"
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/db_xref="GI:54125966"
/tb_ref="di:54125966"
/translation="APTVTLVQLPNGQTVQVHGVIQAAQPSVIQS"
                                                                                                                                                                                                                                                                                77 GGCTGGGCCGCCTGAATAACTCCATGGACTTGAACTGTCTGCCCATTGGGCGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 97)
Parma,D.H., Hicke,B., Bridonneau,P. and Gold,L.
High affinity nucleic acid ligands to lectins
Parent: US 6280932-A 288 28-AUG-2001;
Location/Qualifiers
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Parma, D.H., Hicke, B., Bridonneau, P. and Gold, L. High affinity nucleic acid ligands to lectins Patent: 108 6544959-A 288 08-APR-2003; Gilead Sciences, Inc.; Foster City, CA Location/Qualifiers
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Sequence 288 from patent US 6544959.
AR304919
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Sequence 288 from patent US 6280932.
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="unassigned RNA"
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AR165723.1 GI:16240708
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                                                                                                                 <1. .>92
/gene="CREB"
/number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
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Unclassified.
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Matches 19; Conserve
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Best Local Similarity
Matches 23; Conserv
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AR304919/c
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DEFINITION Sus scrofa cAMP response element binding protein (CREB) gene, exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (20-SEP-2004) Department of Animal Genetics and Breeding,
Agricultural University of Poznan, Wolynska 33, Poznan 60-637,
Poland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                              C07K13/00, A61K37/02, C12N1/21, C12N5/10, C12N15/12, C12N15/70, PC
                                                                                                                                                                                                                                                            25-NOV-1991 JP 1991308976
30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI
TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                              Doi,T., Iwasaki,A., Saino,S., Kimura,S. and Oguchi,M. THROWSIN-EINDING SUBSTANCE AND ITS PRODUCTION PARENT: JP 1994279497-A 12 04-OCT-1994; KOWA CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism='Artificial sequences'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.8; DB 2;
Pred. No. 3.4e+04;
4; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers

    . .63
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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/organism="Sus scrofa"
/wol_type="genomic DNA"
/db_xref="taxon:9823"
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Chmurzynska, A. and Switonski, M.
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JP 1994279497-A/12
04-OCT-1994
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                                                                                              unclassified sequences
                                                                                                                                                                                                                                                                                                                                                                                                topology: Linear;
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illarity 59.0%;
Conservative
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                                   GI:2176374
                                                 JP 1994279497-A/12
                                                                                                                 (bases 1 to 63)
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Sus scrofa
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PN JP 19942
PF 25-NOV-1
PR 30-NOV-1
DDI TAKESHI,
OGUCHI MASAO,
PC COTAIJ/02,
PC (C12NI/2)
CC stranded
CC stranded
CC topology
FH Key
FH Key
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Homo sapiens (human)
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AX898740/c
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PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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I (basea I to 51)
Edwards, J. B.D.M., Duclair, B. and Jordan, J. Y.
Sequence tag and encoded human protein
Parent: JP 2001269182-A 10519 02-OCT-2001;
                                                                                                             31
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24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                     Gaps
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                            24.6%; Score 19.4; DB 2; Length 97; 31.1%; Pred. No. 5.1e+04; Live 16; Mismatches 26; Indels
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                                                                                                                                                                                                                                             linear
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1 (bases 1 to 51)
Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                            BD034273 51 bp DNA Sequence tag and encoded human protein.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
JP 2001269182-A/10519
                                                                                                                                                                                                                                                                                    BD034273.1 GI:22576015
JP 2001269182-A/10519.
Homo sapiens (human)
Homo sapiens
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100 bp mRNA linear ROD 21-JUL-1995
Rattus norvegicus ultraviolet B radiation-activated UV126 mRNA,
partial sequence.
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1 (bases 1 to 100)

1 (bases 1 to 100)

1 (bases 1 to 100)

1 (buthelished pradiation-activated genes induced by transcriptional and posttranscriptional mechanisms in rat keratinocytes

2 (bases 1 to 100)

Rosen C.F.

Rosen C.F.
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 24.3%; Score 19.2; DB 2; Length 51; Best Local Similarity 60.0%; Pred. No. 5.4e+04; Matches 24; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                           51;
Expressed sequence tags and encoded human proteins Patent: US 6783961-A 14603 31-AUG-2004; Genset S.A.;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                           DB 2;
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Best Local Similarity 60.0%; Pred. No. 5.4e+04;
Matches 24; Conservative 3; Mismatches 13
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AX898740
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                                                                                                                                 1. .51
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                                                                                                       Location/Qualifiers
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PAT 06-AUG-2001

linear

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                          Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 271 14 JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.1%; Score 19; DB 2; Length 65; Best Local Similarity 37.5%; Pred. No. 6.7e+04; Matches 15; Conservative 10; Mismatches 15; Indels
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Sequence 271 from Patent WO0142467.
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Job time : 1301 secs
                                                                                                             AXI84576
AX184576.1 GI:15135934
                                                                                                                                                                   Homo sapiens (human)
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Submitted (21-JUL-1994) Cheryl F. Rosen, Medicine, University of Toronto, 100 College Street, Room 317, Toronto, Ontario, MSG 1L5, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-1991 JP 1991308976
30-NOV-1990 JP 90P 335720, 25-FEB-1991 JP 91P 30271 PI
TAKESHI, IWASAKI AKIO, SAINO SUKEYUKI, KIMURA SHIGERU, PI
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Location/Qualifiers
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Doi.T., Iwasaki,A., Saino,S., Kimura,S. and Oguchi,M.
THROMBIN-BINDING SUBSTANCE AND ITS PRODUCTION
THEORIE: JP 1994279497-A 11 04-OCT-1994;
KOWA CO
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Pred. No. 6.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                               40 UGUACUUCGGGCUCGUAUUGUCUCCUCUUCGCCACCUCC 79
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    .65
    /organism="unidentified"
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    /db_xref="taxon:32644"

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JP 1994279497-A/11
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JP 199427947-A/11.
unidentified
unidentified sequences.
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Aad31044 Oligonucl Aat70953 PEGF DNA Aat00367 Family 4 Aat00367 Family 4 Aat09517 Fat antis Adm31245 Rat splic Adm35127 Frobe #16 Aba74927 Human foe Aba39617 Probe #18 Aba39617 Probe #18 Aba39617 Probe #18 Aba39518 Human Dra Aba49195 Human Dra Aba49196 Human gen Acd73164 E. coll K Acd73164 E. coll K Acd73164 Widney di Acd73164 Human Bec Acd73164 Human bre Ada7398 Saccharom Acd73164 Human bre Aba14704 Human bre Aba14731 Human bre Aba1852 Human cer Aah785475 Human cer Aah785475 Human cer Aah72271 Human cer Aah72271 Human cer Aah72271 Human cer Aah72271 Retroelem Adu22177 Retroelem

nucleic

Run on:

Sequence:

Title: Perfect 6

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New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with
                                                                                                                                                                                                                                                                                                  Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                   Human cervical cancer marker nucleic acid 193.
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ACD73164
AAX59388
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ADP49484
AAL24704
AAL24473
ABK36475
AAH71852
AAH68985
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ADU25177
ADU22644
     AAF70953
AAT00367
AAA09070
                                                ABA74927
AAI55452
ABA39617
AAK49572
AAK23422
ABS49195
ABS49195
                                          AA126680
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21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
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21-JUL-2000; 2000US-0220114P.
040W0U44
                                                                                   40188614464411
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                    Schlegel R, Deeds J,
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AAH68919;
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Abg90817 M. capgul
Abd19391 Human RAN
Ada22018 HGF aptam
Adc10528 Human sec
Adm79864 DNA ligan
Abx51458 Bovine ES
Aah68997 Human Cer
Adx69632 Human GnT
Adx69632 Human GnT
Adx69632 Human GnT
Adx696387 Schizosac
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Aaf19666 Human MIP
                                                       alignments)
Million cell updates/sec
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cervical cancer or has a pre-malignant condition; to monitor the grogression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGAGGTACGCGGGGGGTGNAGTAGGCTTCGTCTTCGTCTTCTTCTTCTTCGTTAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         16 GACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCCUUUCGCCAC
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                        Length 97;
                                                                                                                                                                                                                                                                                                                                       26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn tassel-derived polynucleotide (cdps) SEQ ID NO:4883
                                                                                                                                                                                                      Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                     29.9%; Score 23.6; DB 4; 40.6%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 4883; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherman BK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL75509 standard; cDNA; 87 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00294093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0082567P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                           26; Conservative
                                                                                                                                       useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LALGUDI R V.
ITO L Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LALG/) LALGUDI R V. (ITOL/) ITO L Y. (SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lalgudi RV, Ito LY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-163647/21.
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2001051335-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL75509;
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                                                                                                                                                                                                                                                                                                                                           Matches
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ABL75509/
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                                                                                                                                                                                                                                                                                     9 GGGGAGAGACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUU 68
                                                                                                                                                                                                                                                                                                               73 GGGGNGAGTCCGCTGGNAGTTNCCCATGAANNCTATNTNGANCTCGCTCGACCTCGCCGA 14
clone regulatory elements for use in transformation vectors, to express polygeptide, to identify, isolate or extend identical or related corn tassal nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary bypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
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                                                                                                                                                                                                            Score 23; DB 6; Length 87; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                   33; Indels
                                                                                                                                                                          Sequence 87 BP; 17 A; 22 C; 23 G; 15 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANTES receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 53; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                              ch 29.1%;
1 Similarity 43.7%;
31; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0059160P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX54100 standard; DNA; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                  69 UCGCCACCUCC 79
                                                                                                                                                                                                                                                                                                                                                                                        13 ACGTCAGCTCC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cancer; ss
                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX54100;
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conditions or mixtures. The antisense oligonuclectides may be derived from sequences AAX55272-74. These multiple target oligonuclectides diseases and conditions. Typical diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, inflammation, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers and prostate cancer cancer
                                                                                                                                                                                                                                                                                                                                                                                                  GGGCGGGGGAGAGAGCGGCCCCCCTAAATTUGUACTUCGGGCCUCGUAUTGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                           antiallergic; antiasthmatic; cytostatic; analgesic; impaired airwäy; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                        ch 25.8%; Score 20.4; DB 2; Length 86;
1 Similarity 38.6%; Pred. No. 2.9e+03;
27; Conservative 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Low adenosine antisense oligonucleotide SEQ ID NO:1233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                     Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 419; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA33544 Standard; DNA; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 UCCUUUCGCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CCCCBTBGTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-205971/18.
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                             Matches
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The present invention describes a new composition comprising an antisense

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continuerorate (Nat. Aut. 100 was accordance top to 15%), which carges and/or inflammation. The ON can have antilnflammatory, antiallergic, and/or can final analgesic activities. The compositions are antiachmatic. Tycostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary of effects affilict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary vasconstriction, allergies, asthma, compared respiration, respiratory distress syndrome, pain, cystic compared in the cancers which may metastasise to the lungs, including carcinomas, and cancers which may metastasise to the lungs, including carcinomas, and cancers which may metastasise to the lungs, including to breast and prostate cancer. The reduction of the adenosine content of the content of construction and inflammation. AAA32312 to AAA35312 represent the concleotide sequences given in the sequence listing from the present correspond to SEQ ID NO:1 to 2815, and then the last 185 including which correspond to SEQ ID NO:1 to 1690 (AAA32332 to AAA3392) are specifically claimed only from the present invention. N.B. Sequences given in the disclosure of the present invention do not match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Low adenosine antisense oligonucleotide, phosphorothioate, allergy, human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive, antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GGGCGGGGGAGACGACCGCUCUGGCCCCUUAAUUGUACUUCGGGCCUCGUAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with their corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
oligonucleotide (ON) with low adenosine (up to 15%), which targets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MIP-1-alpha/RANTES receptor DNA fragment #1233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF19666 standard; DNA; 86 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Conservative
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61 CCCCBTBGTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 UCCUUUCGCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antisethmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human macrophage inflammatory protein-1-alpha fragment no.1224.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                               25.8%; Score 20.4; DB 3; 38.6%; Pred. No. 2.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                      38.6%; Pred. ....
                                                                                    Claim 14; Page 219; 1592pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ95360 standard; DNA; 86 BP.
                                                                  and respiratory obstructions
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.6%
...rhes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :::| |
61 CCCCBTBGTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 UCCUUUCGCC 73
                                                                                                                                                                                                                                                                                                                                                                             the present invention
                          WPI; 2000-679539/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ95360;
          Nyce JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a computation are subject; for reducing or depleting levels of an antisinflammation bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject; a tissue, or treating bronchocompositicion, cung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed appearance of the printed appearance of the printed appearance of the sequence data for this patent is not represented in the printed appearance of the composition of the printed appearance of the sequence data for this patent is not represented in the printed appearance of the composition of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GGGCGGGGGAGAGAGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katz E, Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 25.8%; Score 20.4; DB 10; Length 86; Local Similarity 38.6%; Pred. No. 2.9e+03; nes 27; Conservative 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 10602; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li Y, Sandrasagra A, K
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                         23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                                                                                                                   24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT69848 standard; DNA; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 UCCUUUCGCC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-229219/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li Y,
                                                                                          WO200285308-A2
    Homo sapiens.
                                                                                                                                                                                    31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT69848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nyce JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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ID AAT6
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AC AAT6
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DT 05-M
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COPEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (II) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with ungivespiratory disorders and malignancies, such as stimulating and activities and malignancies, such as stimulating and activities and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes, binding proteins adhesion molecules and their receptors, cytokines and chemokine receptors, adenosine receptors, bradypinin receptors, crotokine and cransmitters, defensins growth factors, bradypinin respectors, creeptors, cantisense oligonucleotides may be used in this way to treat disorders antisense oligonucleotides may be used in this way to treat disorders and or bronchoconstriction and/or bronchoconstriction and/or particular and/or and/or bronchoconstriction) and/or lung inflammation, allergy (set) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasociated with a disease (CPDE), by pain, cystic fibrosis (CP), allergic rhinitis (AR), pulmonary conditions and/or cancer. ARF18434 to AARF21643 represent human polynucleotide and/or cancer. AARF18434 to AARF21643 represent human polynucleotide in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                              Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GGGCGGGGGAAAGACGGCCCCCUVAAUUGUACUVCGGGCVCGVAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Indels
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0; Gaps

Open circle probe; rolling circle replication primer; mutation detection; amplification target circle; unimolecular segment amplification; multiple target detection; circular DNA; human; cystic fibrosis; ss.

Open circle probe for cystic fibrosis gene.

(first entry)

05-MAR-1998

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Human, antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antififlammatory; antiasthmatic; analgesic; hypotensive; lmmunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; pulmonary hypertension; pulmonary transplantation rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ9016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of
                                                                                                                                                                                                                                                          Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aguilar D;
                                                                                                                                        Eidhammer I, Jonassen I, Jensen HB, Lien T;
Lossius I, Eisen JA, Fraser CM, Durkin AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.1%; Score 19.8; DB 6; Length 93; Best Local Similarity 51.6%; Pred. No. 4.8e+03; Matches 16; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 93 BP; 17 A; 30 C; 26 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GGCACGTTTTTTCACTCCTTTCGGTACCGCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Katz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 GGCUCGUAUUGUCUCUCCCUUUCGCCACCUCC
                                                                             UNIF-) UNIFOB STIFTELSEN UNIV BERGEN
                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 359; 678pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li Y, Sandrasagra A, K
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human RANTES DNA fragment 1224.
                  12-JAN-2001; 2001NO-00000235
12-JAN-2001; 2001NO-00000239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2002; 2002WO-US013143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-2001; 2001US-0286036P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABD19391 standard; DNA; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                      WPI; 2002-557818/59.
                                                                                                                                                                                                                                                                                                                           capsulatus genes.
                                                                                                                                                       Lillehaug JR,
Salzberg SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200285309-A2
                                                                                                                                        Birkeland NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nyce JW, 1
Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABD19391;
                                                                                                  TIGR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a probe to test the method of the invention. The method of the invention is for amplifying a nucleic acid molecule. It comprises mixing at least one rolling circle replication primer (RCRP) with at least one amplification target circle (ATC) which comprises a single stranded circular DNA containing a region complementary to the CRCRP, such that the RCRP hybridises to the ATC and mixing the ATC-RCRP complex with a DNA polymerase and incubating such that a tandem sequence DNA is formed. The method, designated unimolecular segment amplification, is used for detecting specific sequences with high speed and sensitivity. It is especially useful for detecting mutations in genes where numerous distinct mutations are associated with a disease or where mutations in multiple genes are involved. The method is isothermal and provides a simple, consistent amplification occurs not in cycles but as a single continuous reaction. The method is strictly quantitative as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                             Unimolecular segment amplification method for amplifying nucleic acids -uses rolling circle mechanism of amplification, useful for disease-associated genetic mutation(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amplification step is linear and is catalysed by a highly processive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Micro array; gene; ds; differential expression; gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 25.1%; Score 19.8; DB 2; Length 90;
1 Similarity 35.9%; Pred. No. 4.8e+03;
14; Conservative 13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 90 BP; 24 A; 18 C; 12 G; 36 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 CCUUAAUUGUACUUCGGCUCGUAUUGUCUCUCCUUUCG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. capsulatus gene #802 for DNA array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 82; 149pp; English.
                                                                                                                                                                                                 95US-00563912.
96US-0016677P.
                                                                                                                                                         96WO-US018812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2002; 2002WO-NO000019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ90817 standard; DNA; 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methylococcus capsulatus
                                                                                                                                                                                                                                                                                                    Caplan M;
                                                                                                                                                                                                                                                                                                                                         WPI; 1997-298125/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                          (UYYA ) UNIV YALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200255655-A2.
                                   Homo sapiens
                                                                         WO9719193-A2
                                                                                                                                                         21-NOV-1996;
                                                                                                                                                                                               21-NOV-1995;
                                                                                                                                                                                                                    01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
                                                                                                                                                                                                                                                                                                    Lizardi PM,
                                                                                                                 29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2002
                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ90817;
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Gaps

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Sequence 86 BP; 0 A; 26 C; 26 G; 19 T; 0 U; 15 Other;
                                    Claim 15; SEQ ID NO 10602; 763pp; English
                                                                                                                                                                                                                                                                                                                                     HGF aptamers-associated RNA sequence #99
                                                                                                                                                                                                    prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                      ADA22018 standard; RNA; 97 BP.
                                                                                                                                                                                                                        Query Match 24.8%;
Best Local Similarity 38.6%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                           20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                            61 CCCCNTNGTC 70
                                                                                                                                                                                                                                                                  64 UCCUUUCGCC 73
                          bronchodilating agent
WPI; 2003-093058/08
                                                                                                                                                                                                                                                                                                                 ADA22018;
                                                                                                                                                                                                e.g.,
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The invention relates to a purified and isolated non-naturally occurring uncleic acid ligand (an RNA aptamer) to hepatocyte growth factor/scatter factor (HGF) or the HGF receptor, c-met. The ligand comprises a sequence selected from 148 fully defined sequences of 17-101 bp given in the selected from 148 fully defined sequences of 17-101 bp given in the selected from 148 fully defined sequences of 17-101 bp given in the selected from 148 fully defined sequences of 17-101 bp given in the captamer, a method for inhibiting angiogenesis by administering the administering the administering a method for inhibiting of treating the HGF level in an inhibiting tumour comprising the aptamer (and a pharmaceutical excipient), a method for treating a disease of a stansative factor (by a method for inhibiting tumour development acid ligand to HGF) and a method for inhibiting tumour development of a mucleic acid ligand to vascular endothelial factor (VGGF) and/or with a nucleic acid ligands to a teast 2 receptors of growth factors basic fibroblast growth factor, nucleic acid ligands to an least 2 receptors of growth factors in combination with nucleic acid ligands to an least 2 receptors of growth factors in combination with nucleic acid ligands to one or more growth factors.

Combination with nucleic acid ligands to one or more growth factors or nucleic acid ligands are useful as diagnostic and therapeutic agents for hypertension, arreniosclevial myocardial infarction and rheumatoid are useful as diagnostic and therapeutic agents for hypertension, arreniosclevial myocardial infarction and rheumatoid diagnostic information. Nucleic acid ligands that inhibit HGF/c-met interaction are useful for inhibiting tumouriscensis by inhibiting tumouriscensis and motogenesis. The high-affinity nucleic acid ligands coulting the containing modified nuclecties in an individual to obtain prognostic and the containing modified invivo grability or improved delivery containing modified nuclecties end in the papamers when the sequence is an RNA an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40N) surrounded by a constant region. The present sequence is an RNA sequence included in the sequence listing but not mentioned anywhere else
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid ligands to hepatocyte growth factor/scatter factor or c-met, diagnostic and therapeutic agents for hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GAGCGGCUCUGGCCCCUUAAUUGUACUUCGGCCUCGUAUUGUCUCCUCUCCCUUCGCCACCUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             met, diagnostic and therapeutic agents for hypertension, arteriosclerosis, myocardial infarction and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.6%; Score 19.4; DB 9; Length 97; 31.1%; Pred. No. 6.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97 BP; 42 A; 18 C; 27 G; 0 T; 7 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gold L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 101; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Janjic N,
                                                                                                                                                                                                                                                                                                                 95US-00469609.
95US-00536428.
99US-00364539.
                                                                                                                                                                                                         04-FEB-2002; 2002US-00066960.
                                                                                                                                                                                                                                                                                    91US-00714131
                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-2000; 2000US-00502344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GILE-) GILEAD SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .n the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lochrie M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-567063/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                      US2003049644-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 C 79
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Unidentified
                                                                                                                                                                                                                                                                                       10-JUN-1991;
                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
29-SEP-1995;
                                                                                                                                          13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                9-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rabin R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
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                                                                                                                                                                                                                                                                                                                                               comportating oligonucleotides, effective for alleviating because again, comportating oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and bronchoconstriction or respiratory tract inflammation, allergies and cardian adendates of adenominate or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The coligonucleotides are derived from a gene encoding or regulating or regulating dysfunction or cancer and can be anti-sense to the corresponding mRNA.

The invention also describes a kit, that comprises: (a) a delivery of the invention has antiallergic, and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, of the invention has antiallergic, antiinflammatory, antiasthmatic, beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition conspises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The production allammaty observation and/or surfaction and/or lung are asservation and an encompassion of the target mRNA or in the lumps. The second and the administration and/or lung or availability or an encompassion of the production allammation are asserted and an encompassion of the target mRNA or increase the amount observates and an encompassion of the asserted and an encompassion of an encompas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, thilammation, allergies asthma, impeded respiration, respirator, distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ines present in the target RNA serves to prevent the breakdown of igonucleotides into products that free adenosine into the system lung, brain, heart, kidney, etc, tissue environment and thereby, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GGGCGGGGGAGAGAGGAGGGCGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GNGGGGGCNGCNGTTGGGCCCCNNNGGCCCTCTCGTTCNCCTTCTGGCNGTTGCNT 60
                                                                                                                                                                                                                                                                                                                             invention describes a novel composition (a) a first active agent,
                                                                                                            S
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                                                                                                        oligonucleotide containing less percentage of adenosine, targeted trucleic acids associated with lung airway or lung dysfunction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarthritic; gene therapy; cytostatic; RNA aptamer; hepatocyte growth factor/scatter factor; HGF; HGF receptor; c-met; ligand; tumour; angiogeneeis; vascular endothelial factor; VGF; basic fibroblast growth factor; hypertension; arteriosclerosis; myocardial infarction; rheumatoid arthritis; motogenesis; SELEX; systematic evolution of ligands by exponential enrichment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                          Pharmaceutical composition for treating asthma, has antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.6; DB 11; Length 86; Pred. No. 5.5e+03; 7; Mismatches 36; Indels (
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0; Gaps

Indels

78 3 antiasthmatic, cerebroprotective, anti-HIV, virucide, matrix, analytical chemistry, in vivo imaging, blosensor; complex matrix, affinity probe capillary electrophoresis; APCE; ELISA; fibre-optic microarray biosensor; histological marker;

tumour microvessel; anthrax spore; cocaine; ds.

29-MAY-2003; 2003WO-US016796. 31-MAY-2002; 2002US-0384709P. 15-MAY-2003; 2003US-0470750P.

WO2003102212-A2

11-DEC-2003

Unidentified

Synthetic.

Bowser MT, Mendonsa SD; (MINU) UNIV MINNESOTA.

WPI; 2004-043125/04.

CB-SELEX; capillary electrophoresis; ligand-enriched mixture;

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oilgo-dr primed cDNA libraries. Such ESTs are not well suited from oilgo-dr primed cDNA sequences Auch ESTs are not well suited for isolating cDNA sequences CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                             Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 14603; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51 BP; 5 A; 23 C; 19 G; 4 T; 0 U; 0 Other;
                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 14603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression and secretion vectors
                                       ВР.
                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0122487P.
                                     AAC10528 standard; cDNA; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                              EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                 06-OCT-2000
                                                                                                                                                                                                                                                                                                                                     06-SEP-2000,
                                                                          AAC10528;
RESULT 11
                    AAC10528/
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Identifying nucleic acid ligand of target molecule from mixture comprising single stranded nucleic acids having region of randomized sequence by contacting mixture with target molecule, amplifying affinity

Claim 27; SEQ ID NO 6; 90pp; English.

nucleic acids.

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chemistry, useful in wide range of diagnostic assays and as direct chemistry, useful in wide range of diagnostic assays and as direct benefits to many area of the research, including blomedical and health cresearch. Improved aptemers are useful in developing diagnostic assays, for example as diagnostic markers in medical analysis, in vivo imaging and blosensors. The aptemers are used to develop high-sensitivity affinity probe capillary electrophoresis (APCE) assays, in BLISA type assays using enzyme-linked DNA aptemers. Thrombin aptemers be developed for using fibre-optic microarray biosensors. Aptamers against transformed endochellal cells may be selected for use as a histological markers to identify tumour microvessels. Aptamers may be developed for use in other aptamer-based assays, such as assays for analytes ranging from anthrax spores to cocaine. Aptamers having improved quality, improved binding efficiency and selectivity can be identified by the method of the invention. The present sequence is that of an aptamer. DNA sequence which was identified using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel method (CE-SELEX, Capillary Electrophoresis-Systematic Evolution of Ligands by Exponential antichment) of identifying nucleic acid ligands of a target molecule from a candidate mixture comprised of single stranded nucleic acids each having a region of randomised sequence by contacting the mixture with the target molecule, where nucleic acids having affinity to the target molecule, where nucleic acids having affinity to the target molecule, where nucleic acids applicated a ligand-enriched mixture of nucleic acids. The invention may be useful for the production of compounds with an antiasthmatic, cerebroprotective, anti-HIV or virucide activity. The method is useful for identifying nucleic acid ligands of a target molecule from a candidate mixture comparised of single stranded nucleic acids each having a region of randomised sequence. Aptamers identified by the method are useful as a tool in analytical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GCAGCACAGAGGTCAGATGTTGTGTACCGTTATTTGTGCCTCAGCATCCCCGTGGCTAAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 80 BP; 17 A; 21 C; 21 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Conservative
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
24.3%; Score 19.2; DB 3; Length 51;
Best Local Similarity 60.0%; Pred. No. 6.9è+03;
Matches 24; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGAGGGCGGGGGAGAGGAGGGCGCCCCUUAAUU 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 GGGCGGCGGCGCGCAGCAGCTCAGGCCCCTGCAGT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM79864 standard; DNA; 80
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ADM79864;

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Indels 70

24.3%; Score 19.2; DB 8; 37.5%; Pred. No. 7.7e+03; ive 12; Mismatches 13;

Length 87;

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31 CCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUC
                                                          15; Conservative
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                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200142467-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         19-SEP-2001
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                                                                                                                                                                                                                                                                                              AAH68997
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                                                        Matches
                                                                                                                                                                                                           RESULT 14
AAH68997/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 5912 nucleotide sequences, appearing as ABX50072-ABX593, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3, non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid permits the detection of the molecule; and (b) cusplementary nucleic acid permits the detection of the molecule; and (complementary nucleic acid permits the detection of the molecule; and (b) complementary nucleic acid permits the detection of the molecule; and (complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the complementary nucleic acid is used for law of the pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule acid is need for breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 5912 bovine LMFD EXT (expressed sequence was not shown in the specification but was obtained in the borine LMFD acids.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purified nucleic acid molecules, useful for genome mapping, gene identification and analysis, cattle breeding or preparation of constructs for cattle gene expression and genetically improved cattle.
                                                                                                                                                                                                                                                                                                            Bovine, 88; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                               Bovine EST associated with lactation/muscle/fat deposition #1387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 1387; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tao N,
                                                                                                                                                 ABX51458 standard; cDNA; 87 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-2001; 2001US-00983965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0113678P.
99US-00465231.
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BYATT J C.
MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-102386/09
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                          |: :
CTAT 65
COUT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002137160-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998;
15-DEC-1999;
                                                                                                                                                                                                                                    25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                          Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Byatt JC,
                                      62
99
                                                                                                                                                                                            ABX51458;
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                                                                                                    RESULT 13
ABX51458
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Sequence 87 BP; 28 A; 28 C; 3 G; 28 T; 0 U; 0 Other; seqdata.uspto.gov/sequence.html?DocID=20020137160

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-mallygnant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                Cervical cancer; cytostatic; pre-malignant condition; gene therapy; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
40 UGUACUUCGGGCUCGUAUUGUCUCCCUUUCGCCACCUCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65 BP; 19 A; 17 C; 19 G; 4 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 TTTTCTTCGTCNTCGAANANTCTCTTCCTTCGCTNNCGCC
                                                                                                                                                                                                                                                                                                                            Human cervical cancer marker nucleic acid 271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 150; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1999; 99US-0169681P.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-018931SP.
12-MAY-2000; 2000US-0203791P.
09-UJN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.1%;
37.5%;
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Best Local Similarity 37.5
Matches 15; Conservative
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ID ADX6
XX
AC ADX6
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The invention relates to an anti-HM1.24 (I) antibody which has a modified sugar chain. Also included are an antibody composition, containing (I) in which the sugar chain ides not contain fucose and the relative ratio of the sugar chain is 30% or more and producing the antibody. The modified antibody is produced by culturing a host cell in which the ability of the cell to add fucose in the sugar chain of the antibody, is deleted, and in which the nucleic acid encoding the antibody is introduced, by culturing a host cell in which nucleic acid encoding N-acetyl chost cell having both deleted fucose addition ability and ability to express N-acetyl glucosamine transferase III, and extracting the antibody concern the cultured solution. The antibody does not contain alpha-1, 6 core fucose and/or has a sugar chain having a bisecting N-acetylglucosamine (GLONAC) structure. The modified antibody does not contain alpha-1, 6 core tumor and is useful as a therapeutic agent for treating myeloma such as multiple myeloma. The antibody-dependent cellular cytotoxicity (ADCC) of the antibody) is enhanced by the sugar chain modification. The present cellular antibody is a PCR primer used to produce a mutant GnIIII DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-HM1.24 antibody useful for diagnosis of a tumor and useful as a
therapeutic agent for treating myeloma, comprises a modified sugar chain.
                                                                                              Antibody engineering; radioimmunotherapy;
antibody-dependent cellular toxicity;
n-cetyl glucosaminyl transferase III; ss; PCR; primer; Cytostatic;
Immunotherapy; tumor; neoplasm; multiple myeloma; hematological disease;
immune disorder.
                                                            Human GnTIII mutagenic forward PCR primer 1-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugo I, Sugimoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; SEQ ID NO 2; 58pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                          11-AUG-2004; 2004WO-JP011812
                                                                                                                                                                                                                                                                                                                                                                                                                 11-AUG-2003; 2003JP-00207165
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchiya M, Iijima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-173081/18.
                                                                                                                                                                                                                                                                                        WO2005014651-A1
                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                   05-MAY-2005
                                                                                                                                                                                                                                                                                                                                 17-FEB-2005.
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0; Gaps Query Match 24.1%; Score 19; DB 14; Length 97; Best Local Similarity 38.8%; Pred. No. 9.2e+03; Matches 26; Conservative 11; Mismatches 30; Indels Sequence 97 BP; 15 A; 34 C; 16 G; 32 T; 0 U; 0 Other;

72 CCACCUC 78

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63 GCACTTC 69

Search completed: October 16, 2006, 14:32:17 Job time : 305 secs

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BZ381406 SALK 1166 .
CW25897 104 693 1
H25883 y14997 0.51
CW067844 104 315 1
CW067844 104 315 1
CW16703 AV957037 7
CW167293 FLD1 68 C
A1360975 GY02£12.x
AU105862 AU105862
CW022621 104 162 1
DX045680 KBEB047B0
A1539851 CP6510.x
DU099947 JBNY028G0
DU106469 JBNY028G0
DU106469 JBNY028G0
DU106469 JBNY028G0
CR587313 CR587313
AZ605020 1M0671E16
AA691640 v913a07.r
BM157107 fv44d04.y
AK192966 MUS muscu
AA65933 AR182604.s
CB046583 NISC G£05
DY248960 CSTFBID04
CD945332 RDX.Z Gen
BJ029975 GY029975
                                                                                                                                                                                                                                                                                                          BX728792 SGC-tadpole Xenopus tropicalis cDNA clone TTpA036j08 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Croning MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS EXQUENCE ID: TTPA036j08.plkSP6
Sequenching primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
CDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
embryos. ECORI.NotI cut CDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site_1: ECORI; Site_2: NotI
Host: Escherichia coli DH108.
                                                                                                                                                                                                                                                                                                                                                                              Eukaria Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukabibia; Metazoa; Chordata; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 76)

1 (Croling, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (11_2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                                                                                                                                                                ALIGNMENTS
                            CW067844
AV957037
CO167293
AU360975
AU30862
CW022621
DX045680
AI339851
DU099947
DU106469
BX289701
CR587313
AZ605020
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AX692983
CB046583
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BX728792
BX728792.1 GI:38401533
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COMMENT
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BX728792
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  A1583881 tt70564.x
A1589698 qw89f06.x
BQ382202 kk43803.y
BF147704 us40a01.x
A1616438 zehn0074.
CG13143 XB629 Bay
H5538 CHR220577 C
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1021.181 Million cell updates/sec
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                                                                                                                     1 ggagggggggggagacga.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                      853524
                                                                                                                                                                   48236798 segs, 27959665780 residues
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
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                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length DB
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Maximum DB seq length: 100
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Database :

Result No.

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Sequence:

Run on:

Searched:

AZ769498 1M0570K16 CR076775 Reverse s DN441479 LIB5338-1 AJ649396 AJ649396 AA437593 vd05£03.8

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

I (bases 1 to 91)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,

M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CONG distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALEUDOUS SET 17-NOV-1998 WW99f06.x1 NCI CGAP Brn35 Homo sapiens CDNA clone IMAGE:1998275 3' ALEGEGS A ALEGEGE TO TR:014934 014934 NF-AT3. ; mRNA sequence.
                                                               AI583881 51 OCAPP. 191 bp mRNA linear EST 06-APR-199 CH-70b04.x1 NCI CGAP HSC3 Homo sapiens CDNA clone IMAGE:2246095 3' similar to TR:063624 Q63624 CTD-BINDING SR-LIKE PROTEIN RA1. contains element TAR1 TAR1 repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GGAGGAAGGAACGAAGGTCCTGCTTTTCTTTTCTCTNCCCCTTTCTTTCTTTTCTTTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib. WINCI CGAP HSC3"
//note=Torgan: NCI CGAP HSC3"
//note=Torgan: NCI CGAP HSC3"
//note=Torgan: None marrow; Vector: pAMP1; mRNA made from lymphoid tissue, cDNA made by oligo-dr priming.
Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA Library Preparation: David B.
Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research S6:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 gacagagagagagacagacagacacacatuaatuuguacuucagacucguauugucucu
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Seg primer: -400P from Gibco
High quality sequence scop: 1.
Location/Qualifiers
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Homo sapiens
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1 (bases 1 to 84)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., La, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:476265
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            AA414137 STOWLES SOLTER MOUSE 2 CELL MUS MUSCULUS CDNA CLONE LIMAGE: 791857 5', mRNA sequence.
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                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                            Length 76;
                                                                                                                                      9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CUUDANUIGUACUUCGGGCUCGUAUUGUCUCCUUU 69
                                                                                         27.3%; Score 21.6; DB 4;
41.7%; Pred. No. 1.6e+04;
iive 12; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J x DBA/2J
/db_xref="taxon:10090"
/clone="IMAGE:791857"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                 AA414137.1 GI:2074294
                                                                                                                                        15; Conservative
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Matches 17; Conserv
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                                                                                              Query Match
Best Local (
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                  RESULT 2
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Gaps

64

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Contact: Mccarter JP
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter at Washington University, St. Louis. The cDNA was made by
using Dynabead oligo-dr priming (Dynal). PCR based library using a
modified protocol from the SMART PCR cDNA Synthesis Kit from
Clontech. Directionally cloned into the UDG sites of pAMP1.
Dissected nematode tissues were provided by Dr. Alan Scott
(ascott@jhsph.edu) of the School of Public Hygene and Public Health
at John Hopkins University in Baltimore, MD.
Seg primer: T7 from Gibco
High quality sequence stop: 99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jobes "Vector: pAMP1 (Gibco); Site 1: Not1; Site 2: Sal1; The library was constructed by Brandi chiapelli and Dr. James McCarter at Washington University, St. Louis. The CDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR CDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@insph.edu) of the School of Public Hygene and Public Health at John Hopkins University in Baltimore, MD."
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1 (Dass 1 to 85)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 GAGAGACGAGCGCCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGCTGCTGGCGCTCCAGCCAACTTACTGAACTTCAGAAGCGTTTCGTGCCTACGATC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Intestine"
/dev stage="Adult"
/dab_hose="BH10B"
/clone_lib="Ascaris suum male gut pAMP1 v2 Chiapelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.1%; Score 20.6; DB 3; Length 100; 42.4%; Pred. No. 3.7e+04; tive 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Ascaris suum"
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Othorblished (1997)
Othor ESTs: us40a01,y1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:6253"
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                                 McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
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BF147704/C
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbe-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R..
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCICGAP_Brn35"
/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningiona, oligodendroglioma, astrocytoma (grade II),
medulloblastcma, astrocytoma (grade IV). Life Technologies catalog #: 11544-012"
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                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 91)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 100)

McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="tumor, 5 pooled (see description)"
/lab host="DH10B"
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Eukaryota, Metazoa, Nematoda, Chromadorea, Ascaridida,
Ascaridoidea, Ascarididae, Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality
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Location/Qualifiers
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/db_xref="taxon:9606"
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                                                            Homo sapiens
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musculus
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nes 17; Conserv
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Best Local Similarity
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VERSION
KEYWORDS
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                      Matches
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                       /dev_stage="embryo, 10.5 dpc"
/lab_host="DH10B (phage resistant)"
/lab_host="DH10B (phage resistant)"
/looe="Vector: pr7730-Pao1; Site_1: Not1; Site_2: EcoRI;
/note="Vector: pr7730-Pao1; Site_1: Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 21-APR-1999
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eDN0074.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG 3'
Seg primer: 5' GAAATTAACCCTCACTAAAGGG 3'
                                                                                                                                               Trace considered overall poor quality Possible reversed clone: polyr not found High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    'tissue_type="branchial arches"
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Harvard Medical School
Francis St. Boston, MA 02115, USA
Tel: 6177228915
                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3169512"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cliew@rics.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI616438.1 GI:4625605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Liew CC
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                                                                                                                            MGI:1064972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on, C.
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KEYWORDS
SOURCE
ORGANISM
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AI616438/c
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                                                                                                                                                                                                            FEATURES
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XE629 BayGenomics Gene Trap Library pGT1Lxf Mus musculus CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XE629
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                                                                                                                                                                                                    CDNA was
mer. EcoRI
                                       /dev_stage="embryonic day 3 post-fertilization"
/lab_bost="E.coli XL1-Blue mrF" |
/clone lib="Zebrafish Embryonic Heart cDNA Library"
/clone lib="Zebrafish Embryonic Heart cDNA Library"
/clone lib="Zebrafish Embryonic Heart CDNA Library"
/clone lib="Zebrafish Embryonic Hearts (3 day post-fertilization). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. ECORI adaptors were ligated, followed by digestion with XhoI, for directional cloning into pre-digested lambda ZAP
Express vector. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGAGGGGGGGGAGAGAGAGGGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 GGGGCTCGGGGGCTCCTGGCGGAATCCTCTGAAAGGCCCTTCCGCCGGGGCGGG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: BayGenomics
Bay Area Punctional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
equence tag generated by 5' RACE of total RNA from gene trapectl lines. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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/clone lib="BayGenomics Gene Trap Library pGT1Lxf"
/note="Vector: pGT1Lxf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 ugaccccuuaauuguacuucgagcucguauugucuccuuucgccaccucc 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                      ch 25.6%; Score 20.2; DB 1; Length 100; 1 Similarity 45.2%; Pred. No. 5e+04; 33; Conservative 7; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 81;
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    .81
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="129 ola"

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/sex="Male"
mol_type="mRNA"
db_xref="taxon:7955"
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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CC183143.1 GI:30427043
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Class: Gene Trap.
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Gaps .; 0

Indels

79

Length 78;

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Inote="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, deforted repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electropozated into E. coli cells. This is a methylation filtered library."
This sequence was generated from the T7 end of BAC 438014. 438014 is part of the CH012-242 BAC Library created by P. de Jong. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CW115558 19-0CT-2004 104 490 11106626 116 34591 001 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11106626, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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/culfivar="ATx623"
/db_xref="taxon:4558"
/clone="1110626"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 83)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | : | : | | : | | | : | 47 CATGAAATGAATTTTAGAGCTCC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 CCUDAAUUGUACUUCGGGCUCGUAUUGUCUCCUCCUUUCGCCACCUCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbdell@coriongenomics.com
Plate: 490 row: o column: 02
Seq primer: T3 Reverse
Class: mechylation filtered
High quality sequence stop: 83.
                                                                                                                                       1.78
/organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="CH2424-38014"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.1%; Score 19.8; DB 14; Best Local Similarity 38.3%; Pred. No. 6.8e+04; Matches 18; Conservative 12; Mismatches 17;
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Sorghum bicolor
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CW115558.1 GI:54808105
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DEFINITION
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/clone lib="Chromosome 22 exon"
/clone lib="Chromosome 22 exon"
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/note="Vector: pBluescriptIKS+"
/note: pBluescriptIKS+"
/note="Vector: pBluescriptIKS+"
/note: pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 88)
Trofatter, J. J., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F.
and Buckler, A.J.
An expression-independent catalog of genes from human chromosome 22
Genome Res. 5 (3), 214-224 (1995)
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Humphray, S. J., Plumb, R.W. and Durham, J.L.
Direct Submission

Direct Submission

Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
                                                                                                                                       H55638 18 bp mRNA linear EST 07-DEC-1995
CHR220577 Chromosome 22 exon Homo sapiens cDNA clone C22_783 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Fax: 6177249616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 UGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: buckler@helix.mgh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                    H55638.1 GI:1108504
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Buckler AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .88
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T3.
                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                    LOCUS
DEFINITION
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CT351516/c
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PUBMED
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                                                                                                        155638/c
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CW115559

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CW020424 11 bp mRNA linear GSS 28-SEP-2004
GC0686 TIGEM gene trap library Mus musculus cDNA clone A011.64,
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PCRS50390_2 Hematopoietic stem cells Mus musculus CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +3908165132205
Fax: +390815790919
Fax: +300815790919
Fax: +300815790919
Fax: +300815790919
Fax: +300815790919
Fax: +300815790919
Fax: +300815790919
Fax: +3008159081.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
available upon request from TIGEM. Annotation information
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                            Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Barbarishi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
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1 (bases 1 to 84)
Priteker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGAGGGGGGGGAGAGAGGGGCCUCUGGCCCCUUAAUUGUACUUCGGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 24.8%; Score 19.6; DB 13; Length 71; I Similarity 52.0%; Pred. No. 7.8e+04; 26; Conservative 5; Mismatches 19; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Embryonic stem cell"
|cell_line="Ell4"
|colo_lil="TIGEM gene trap library"
|note="Vector: pFLIP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/clone="A011.G4"
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Mus musculus
                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                           CW020424.1 GI:52789684
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                                                                                                                                                                             mRNA sequence.
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     75 TCT 77
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Best Local S:
Matches 26
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AUTHORS
                                                                         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                       CW115559 11106626 148 34587 001 Sorghum methylation filtered library (LibID: 104) Sorghum Dicolor genomic clone 11106626, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAGGGCGGGGGAGGAGCGGCCCCCUUAAUUGUACUUCGGGCUCGUAUUGUC 61
                                                                                                                               1 (bases 1 to 83)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martienssen,R.A.
                                                                                                      2 GAGGCCGGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUC
                                                        Gaps
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Score 19.8; DB 13; Length 83;
Pred. No. 6.8e+04;
8; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
11-13 14 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: jbedell@oriongenomics.com
Plate: 490 row: o column: 02
Seg primer: SWfor Porward
Class: methylation filtered
High quality sequence stop: 83.
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/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:4558"
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Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CW115559.1 GI:54808106
Query Match 25.1%;
Best Local Similarity 44.4%;
Matches 28; Conservative
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7 TCT 5
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Roslin, Midlothian, EH2S 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
V0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptil(KS) R. Sitel: ECORI
R. Site2: Not1 5' Seq Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH2S 9PS, www.ark-genomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
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/mol type="mmkh"
/db xref="taxon:9823"
/db xref="taxon:9823"
/tissue type="covary"
/clone lib="CSEQRAN19"
/note="voctor: pBlueScript11(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
Diversification of Stem Cell Molecular Repertoire by Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCUUUCGCCACCUC 78
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                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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/tisuse_type="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/clone_lib="Hematopoietic stem cells"
/note="ColMA library was made from FACS-purified hematopoietic stem cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                      Contact: Pritsker M
Lab of Ihor Lemischka, Department of Molecular Biology
Princeton University
Princeton 103844, USA
Tel: 609 258 5657
Fax: 609 258 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
24.8%; Score 19.6; DB 10; Length
Best Local Similarity 36.2%; Pred. No. 8e+04;
Matches 21; Conservative 13; Mismatches, 24; Indels
                                                Proc. Natl. Acad. Sci. U.S.A. (2005) In press
                                                                                                                                                                                                                                Email: pritsker@molbio.princeton.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ649396.1 GI:49326241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                           Splicing
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AJ649396
LOCUS
DEFINITION
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                           FEATURES
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TITLE
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ORIGIN

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        Query Match
        24.8%; Score 19.6; DB 1; Length 85;

        Best Local Similarity 42.0%; Pred. No. 8e+04;

        Matches 21; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

        Qy
        16 GAGAGGGCUGGGCCCUNANUGACUUCGGGCCUGUAUUGUCUCUC 65

        Qy
        | | | | | | | | | | | | |

        Db
        8 GTCGGGAGGCCTGCCTCCTCCTCCTCCTCCTCCTCTC 57
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Search completed: October 16, 2006, 16:16:48 Job time: 4331 secs

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIPICATION: UNKNOWN
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: AMESI, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1233:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1233:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 86 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Appl
Sequence 12, Appl
Sequence 288, App
Sequence 288, App
Sequence 14603, A
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       753, App
415, App
27, Appl
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28, Appl
86, Appl
16, Appl
16, Appl
16, Appl
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Sequence 18431, A
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Appl
Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1seued Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/T_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*
0: /EMC_Celerra_SIDS3/ptodata/2/ina/PC_COMB.seq:*
0: /EMC_Celerra_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CELERRA_SIDS3/ptodata/2/ina/PC_CEL
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  5.1.9
Biocceleration Ltd.
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US-08-488-031-16
US-08-486-569-16
                                                                                                                                                                                                                                                                                                                                                                             1403666 segs, 935554401 residues
GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                      nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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79
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Match
                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                           Scoring table:
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118.8
118.4
118.4
128.1
13.2
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24 18 22.8 78 2 US-08-488-027-16 Sequence 16, Appl	25 18 22.8 78 2 US-08-09-16 Sequence 16.	27 18 22.8 78 3 US-08-482-658-16 Sequence 16,	28 18 22.8 78 3 US-08-470-349-16 Sequence 16,	29 18 22.8 78 3 US-08-475-610-16 Sequence 16,	30 18 22.8 78 7 PCT-US92-00277-16 Sequence 16,	31 18 22.8 78 7 PCT-US92-00278-16 Sequence 16,	17.8 22.5 77 5 US-09-844-508-25 Sequence 25,	3 17.8 22.5 87 3 US-09-873-075A-5 Sequence 5,	4 17.8 22.5 87 4 US-09-393-803-68 Sequence 68,	5 17.6 22.3 50 3 US-10-131-827-847 Sequence 84°	6 17.6 22.3 50 5 US-10-131-831-847 Sequence 84 ^o	7 17.6 22.3 59 2 US-08-790-963-53 Sequence 53,	8 17.6 22.3 59 3 US-09-371-774-53 Sequence 53,	9 17.6 22.3 59 3 US-09-875-082-53 Sequence 53	40 17.4 22.0 72 2 US-08-433-126A-13 Sequence 13,	41 17.4 22.0 72 2 US-08-433-124A-13 Sequence 13,	42 17.4 22.0 72 3 US-08-976-413A-13 Sequence 13.	3 17.4 22.0 72 7 PCT-US96-06059-13 Sequence 13.	44 17 4 22 0 91 3 US-09-513-999C-15862 Sequence 1586	45 17.2 21.8 54 3 US-09-621-976-13448 Sequence 1	RESULT 1	US-U9-543-679A-1233 : Semience 1233. Application US/09543679A	Patent No. 7034007	GENERAL INFORMATION:	TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONOCLEDITLE.	ODDEDS ASSOCIATED	LUNG INFLA	NUMBER OF SEQUENCES: 3111	ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.	STREET: 7 Clarke Drive	: CITY: Cranbury	STATE: NO	COUNTY: USA	COMPUTED DESCRIPE FORM.	MEDIUM TYPE: CD-R	Σ	SYSTEM: DOS	SOFTWARE: N/A
2.0	4 (1 (1	7	~	٣	m	32	33	'n	35	36	37	38	39	4	4	4	4	4	4	RESULT	75-09-SU	Patent	GEN						•								

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APPLICANT: Doi, Takeshi
APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
CORRESPONDENCES: 18
CORRESPONDENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.1%; Score 19.8; DB 2; Length 6 Best Local Similarity 59.0%; Pred. No. 5.6e+02; Matches 23; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110, Oll APPLICATION NUMBER: US/08/110, 011A
FILING DATE: 23-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5384664man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-073-0 DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 AGGTCGACGACGAGGCCACCAGCGCTCTGGCGACTGACTCG
                                                                                                                                                                                                                                                 80-071-0 CIP
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435
                                                                    CLLING
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-071-
TELEPHONE: (703)413-220
TELEPAX: (703)413-220
TELEFAX: (703)413-220
TELEXX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENATION FOR SEQ ID NO: 12:
LENGTH: 63 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-110-011A-12/c
; Sequence 12, Application US/08110011A
Patent No. 5354664
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703)413-3000
TELEFAX: (703)413-220
TELEX: 246855 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENTH: 63 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-014-723-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
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APPLICANT: Saino, Yushi
APPLICANT: Saino, Yushi
APPLICANT: Kimura. Shigeru
APPLICANT: Kimura. Shigeru
APPLICANT: Chuchi, Masso
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                    25.8%; Score 20.4; DB 5; Length 86; 38.6%; Pred. No. 3.6e+02; tive 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlinginia STATE: Virginia STREE: Virginia STREET: Alsonia STREET: Virginia STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18431, Application US/09621976

Batent No. 6639063

GENERAL INPORMATION:
APPLICANT: Johnas Mine Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
TITLE OF INVENTION UNBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 18431
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 GCCGGGGAGAGACGACGCCCUUGGCCCCUUAAUU 40
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Best Local Similarity 63.9%; Pred. No. 5.2e+02;
Matches 23; Conservative 3; Mismatches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-08-014-723-12/c
Sequence 12, Application US/08014723
Patent No. 5273962
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 63..64,83
OTHER INFORMATION: n=a, g, c or t
                                                                        Query Match
Best Local Similarity 38.6%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doi, Takeshi
Iwasaki, Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                          64 UCCUUUCGCC 73
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61 CCCCBTBGTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-621-976-18431/C
       US-09-543-679A-1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-621-976-18431
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Gaps ö

Length 63;

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90 GTGAGCCTCCTGTCGAATCTTACTACTTCTGCTTTGTGTTTTGTTTTCCTTGCGTGCCCTT 31
                                                                                              19 GAGCGGCUCUGGCCCCUUAAUUGUACUUCGGCCUCGUAUUGUCUCCUCUUUCGCCACCUC
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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24.6%; Score 19.4; DB 3; Length 97; ilarity 31.1%; Pred. No. 8.9e+02; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                   Sequence 288, Application US/09849928
Patent No. 6544959
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
APPLICANT: PARMA, TOH APPINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: All C'8 are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) SEQUENCE DESCRIPTION: All U's are 2'-NH2 uracil ; SEQUENCE DESCRIPTION: SEQ ID NO: 288: US-09-849-928-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/849,928
FILING DATE: 04-May-2001
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/952,793
FILING DATE: «Unknown-
APPLICATION NUMBER: 08/479,724
FILING DATE: 07.-UNB-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07.-UNB-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07.-UNB-1995
APPLICATION NUMBER: 08/47,829
FILING DATE: 07.-UNB-1995
FILING DATE: 07.-UNB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 288: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 19; Conserva
                          Best Local Similarity
Matches 19; Conserv
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       Query Match
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                                                                                                                                            Gaps
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                                                                                                Length 63;
                                                                                            Query Match 25.1%; Score 19.8; DB 2; Length 6. Best Local Similarity 59.0%; Pred. No. 5.6e+02; Matches 23; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 288, Application US/08952793
Patent No. 6280932
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
                                                                                                                                                                                          41
                                                                                                                                                                                                                  40 AGGICGACGAGGCCAGCGGCICTGGCGACTGACICG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: ISM pc compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        All C's are 2'-NH2 cytosine
                                                                                                                                                                                        3 AGGCCGCGCGAGAGACGAGCGCCUCUGGCCCCUUAAUUG
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US-08-952-793-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPLICATION NUMBER: 08/4/2,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY AGENT INFORMATION:
NAME: BARTY J. SWAINSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELECHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/952,793
    Other nucleic acid;
DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATE: APPLICATION NUMBER: 08/472,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 97 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Englewood
Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
; MOLECULE TYPE:
; DESCRIPTION:
US-08-110-011A-12
                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-952-793-288/c
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US-09-13-999C-14603/C

i Sequence 14603, Application US/09513999C

i Sequence 14603, Application US/09513999C

i Sequence 14603, Application US/09513999C

i Betent No. 6783961

i APPLICANT: Dunmas Milne Edwards, J.B.

i APPLICANT: Duclert, A.

i APPLICANT: Glordano, J.Y.

i TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PALENE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 14603

LENGTH: 51

LENGTH: 51
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APPLICANT: Iwasaki, Akio
APPLICANT: Saino, Yushi
APPLICANT: Kimura, Shigeru
APPLICANT: Kimura, Shigeru
APPLICANT: Ohkuchi, Masao
TITLE OF INVENTION: Thrombin-Binding Substance and Process
TITLE OF INVENTION: For Preparing the Same
CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%; Score 19.2; DB 3; Length 51; 60.0%; Pred. No. 8.9e+02; tive 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGAGGGGGGGGAGAGACGAGCGGCUCUGGCCCCUUAAUU 40
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REFERENCE/DOCKET NUMBER: 80-071-0 CIP
FELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Fatentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,723
FILING DATE: 19930208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Oblon, No. 5273962man F.
REGISTRATION NUMBER: 24,618
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 11, Application US/08014723
; Patent No. 5273962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0%
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-513-999C-14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
79 C 79
                                                                30 C 30
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                                            19 GAGCGGCUCUGGCCCCCUDAAUUGUACUUCGGCUCGUAUUGUCUCUCCCUTUCGCCACCUC 78
   90 GTGAGCCTCCTGTCGAATCTTACTACTTCTGCTTTGGTTTTGTTTTGTTTCCTTGCGTGCCCTT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.6%; Score 19.4; DB 7; Length 97; Best Local Similarity 31.1%; Pred. No. 8.9e+02; Matches 19; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compartible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
FILING DATE: 05 JUNE 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                              PCT-US96-09455A-288/C
Sequence 288, Application PC/TUS9609455A
GENERAL INFORMATION:
TITLE OF INVENTION: LIGANDS TO LECTINS
TITLE OF INVENTION: LIGANDS TO LECTINS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratechun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: All U's are 2'-NH2 uracil
PCT-US96-09455A-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Swanson & Bratschun, L.L.C.
F: 8400 E. Prentice Avenue, Suite 200
Englewood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: 08/477,829
FRIOR APPLICATION NUMBER: 08/477,829
FRIOR APPLICATION NUMBER: 08/477,829
APPLORATE OATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: 08/477,829
ATTORNEY OATE: 07-JUNE-1995
ATTORNEY OATE: 07-JUNE-1995
ATTORNEY OATE: 07-JUNE-1995
ATTORNEY OATE: 07-JUNE-1995
ATTORNEY OATE: 03/3133
TELECOMMUNICATION INFORMATION:
TELECOMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colorado
                                                                                                                                    79 C 79
                                                                                                                                                                                                 30 C 30
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30 AGGTCGACGACGAGGCCAGCGGCTCTGGCGACTGA 64
                                                                                                                                                  US-09-367-791A-19; Sequence 19, Application US/09367791A; Patent No. 6573071; Patent No. 6573071; GENERAL INFORMATION:
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415) 576-0300
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SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.7<sup>3</sup>
Matches 17; Conservative
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셤
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Patent No. 5354664
GENERAL INFORMATION:
APPLICANT: Doi, Takeshi
APPLICANT: Saino, Yushi
APPLICANT: Saino, Yushi
APPLICANT: Shigeru
APPLICANT: Mimura Shigeru
APPLICANT: Mimura Shigeru
APPLICANT: Pinvention: Thrombin-Binding Substance and Process
TITLE OF INVENTION: Por Preparing the Same
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia SIR: Virginia Virg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.1%; Score 19; DB 2; Length 65; 62.9%; Pred. No. 1.18+03; tive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/110,011A
FILING DATE: 23.AUG-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
24.1%; Score 19; DB 2; I
Best Local Similarity 62.9%; Pred. No. 1.1e+03;
Matches 22; Conservative 3; Mismatches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AGGCGGGGGAGACGAGCGGCUCUGGCCCCUUA 37
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ER: 80-073-0 DIV
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NAME: Oblon, No. 5354664man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 60-073-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3200
TELEFAX: (703)413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-014-723-11
                            INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 65 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.9 Matches 22; Conservative
(703)413-2220
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-110-011A-11
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TELEFAX:
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3 AGGCCGCGCGCACCAGCGCCCCCUVA 37

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APPLICANT: Himmelspach, Michele
Schlokat, Uwe
Schlokat, Uwe
Dorner, Friedrich
Fisch, Andreas
Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.8%; Score 18.8; DB 3; Length 39; 44.7%; Pred. No. 1.2e+03;
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US-08-444-818-753/c
Sequence 753, Application US/08444818
Fatench No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: William J.
NUMBER OF SEQUENCES: 777
                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPEs Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FactSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 CCUUDANTUGUACUTCGGGCUCGUAUTGUCUCCUCCUTUC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/367,791A
PILING DATE: 12-No. 6573071-1999
CLASSIPICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATE:
TLING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
PILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-367-791A-19
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Query Match
Best Local Similarity
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67 TC 68
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Patent No. 6177557

GENERAL INPORMATION

APPLICANT: Janjic, Nebojsa

APPLICANT: Tasset, Dianne

TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC

TITLE OF INVENTION: FIRROBLAST GROWTH FACTOR AND

TITLE OF INVENTION: THROMBIN

NUMBER OF SEQUENCES: 445

CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: IBM compatible OPERATION SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA: FILLING DATE: 08-MAY-1996 CLASSIFICATION: 435
                                                                                                                                                                                         ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
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8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: HARNIN, Allsa A.
REGISTAATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEPHONE: (5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer JHC 13"
US-08-444-818-753
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
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Best Local Similarity
                                                                  STREET: 4560 Hort
CITY: Emeryville
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: USA
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STATE: Colorado
                                                                                                                                                                        USA
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STREET: 84
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US-08-687-421-415
                                                                                                                                                                    COUNTRY:
                                                                                                                                     STATE:
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Sequence 27, Application US/08965762

GENERAL INFORMATION:
APPLICANT: KOltin, Yigal
APPLICANT: Gavrias, Victoria
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 07334/062001
CURRENT APPLICATION WUMBER: US/08/965,762
CURRENT APPLICATION UNMER: 1997-11-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PRESENCE for Windows Version 3.0
SEQ ID NO S. 35
LENGTH: 62
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Best Local Similarity 38.7%; Pred. No. 1.4e+03;
Matches 24; Conservative 11; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.3%; Score 18.4; DB 3; 38.5%; Pred. No. 1.9e+03; tive 11; Mismatches 21;
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION NUMBER: 08/195,005
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION NUMBER: 07/97,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION NUMBER: 07/97,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA: 07/314,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA: 07/35,428
FILING DATE: 11-JUNE-1991
APPLICATION NUMBER: 07/714,131
FILING DATE: 11-JUNE-1991
APPLICATION NUMBER: 33,215
REGISCHAUMICATION NUMBER: 33,215
REGISCHAUMICATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXO7/PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae US-08-965-762-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ 1D NO: 41.
SEQUENCE CHARACTERISTICS:
LENGTH: 79 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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RESULT 15
US-09-911-927-27
Sequence 27, Application US/09911927
Fatent No. 6461826
GENERAL INFORMATION:
HOWATION:
HOWATION:
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HOWBER:
HOWELL ATTING DATE:
HOWATE:
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Search completed: October 16, 2006, 14:34:12 Job time : 111 secs

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-310-914A-16611/c
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-16611
                                               Best Loc
Matches
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11. /ERC Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCONB.seq:*

22. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCONB.seq:*

33. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCONB.seq:*

44. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCONB.seq:*

45. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCONB.seq:*

46. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCONB.seq:*

47. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCONB.seq:*

48. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCONB.seq:*

49. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCONB.seq:*

40. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCONB.seq:*

40. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCONB.seq:*

40. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCONB.seq:*

41. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

42. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

43. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

44. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

45. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

46. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

47. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

48. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

48. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*

48. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCONB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4883, Ap Sequence 288, App Sequence 288, App Sequence 288, App Sequence 288, App Sequence 1387, App Sequence 22, Appl Sequence 22, Appl Sequence 17212, A Sequence 15, Appl Sequence 15, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Appl
Sequence 3, Appli
Sequence 3993, Ap
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                                                                                                          , Search time 881 Seconds
(without alignments)
1101.842 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                           1 ggagggggggggagagacga......ucucuccuuucgccaccucc
             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-02-94-0918-4883

US-0-849-928-88

US-10-066-960-288

US-10-409-627-288

US-10-409-627-288

US-10-498-250-6

US-10-983-965-1187

G US-11-106-909-22

G US-11-228-636-23

US-10-918-35-21

US-10-918-35-21

US-10-918-37-12

US-09-918-40-15

US-10-835-516-15
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US-10-853-774-3
US-09-908-975-3993
                                                                                                                                                                                                                                                                                         18892170 segs, 6143817638 residues
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           nucleic search, using sw model
                                                                                                           October 16, 2006, 14:32:38
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 100
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                                                                                                                                                                          Title:
Perfect score:
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199.4
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Sequence 16611, Application US/10310914A

Publication No. US2060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION:
USES thereof
TITLE OF INVENTION:
USES thereof
TITLE OF INVENTION:
USES THE REFERENCE:
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 16611
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NS-09-294-093B-4883/C
Sequence 4883, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Laludi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENEUR: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL;
FILE REPERENCE: PL-0009 US;
CURRENT APPLICATION NUMBER: US/09/294,093B
                                                                         Sequence 27, Appl Sequence 27, Appl Sequence 1520, Appl Sequence 1520, Appl Sequence 10452, A Sequence 931, Appl Sequence 331, Appl Sequence 21, Appl Sequence 21, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 36, Appl Sequence 25, Appl Sequence 36, Appl Sequence 363, Appl Sequence 363, Appl Sequence 363, Appl Sequence 25, Appl Sequence 363, Appl Sequence 372387, Sequence 976170,
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Sequence 8102, Ap
Sequence 29840, A
                            Sequence 173876, Sequence 47265,
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Pred. No. 6.8;
2; Mismatches 5; Indels
                                                                         US-09-911-888-27

US-09-911-927-27

US-10-910-9144-15206

6 US-11-175-85-73819

US-10-918-975-10452

US-10-918-975-10452

US-10-918-975-91

US-10-956-734-314

US-10-396-734-28

US-10-396-734-28

US-10-384-284-284

US-10-384-286-25

I US-09-844-586-25

I US-09-844-586-25

I US-09-87-0754-5

I US-09-87-0754-5

I US-09-87-0754-5

I US-09-728-445-363

I US-10-964-549-363

I US-10-964-549-363

I US-11-036-317-296412

I US-11-036-317-27287
                                     US-10-932-182A-173876
US-11-175-859-47265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-175-859-8102
US-11-175-859-29840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
34.2%;
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79 C 79
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                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 GGGGAGAGAGAGGGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCUU 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature;
CTHER INFORMATION: Incyte ID No. US20010051335A1 700355274H1
NAME/KEY: unsure;
LOCATION: 32, 35, 37, 42-43, 52, 57, 69, 79, 81
COTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: PARKA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 390
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.1%; Score 23; DB 3; I Best Local Similarity 43.7%; Pred. No. 2.2e+02; Matches 31; Conservative 7; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICATION DAMER: US/09/849,928
FILING DATE: 04 May-2001
CLASSIPICATION: CURKNOWN>
PRIOR APPLICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,793
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-UNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-UNE-1995
APPLICATION NUMBER: 08/472,255
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-UNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-UNE-1995
APPLICATION NUMBER: 08/477,829
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REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 4883
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-849-928-288/c
'Sequence 288, Application US/09849928
'Publication No. US20030059769A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 793-3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 UCGCCACCUCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ACGTCAGCTCC 3
                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                            FEATURE:
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19 GAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCCUUUCGCCACCUC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.6%; Score 19.4; DB 3; Length 97; Best Local Similarity 31.1%; Pred. No. 5.1e+03; Matches 19; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dilication No. COLORDO SENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO LECTINS
                                                                                                                                                                                                                                 OTHER INFORMATION: All C'8 are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
                                                                                                                                                                                                                                             OTHER INFORMATION: All U's are 2'-NH2 uracil sequence DESCRIPTION: SEQ ID NO: 288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 390
CORRESPONDENCE BADRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM DC COMPATIBLE
COMPATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/066,960
FILING DATE: 04-Feb-2002
CLASSIFICATION NUMBER: US/20/2
APPLICATION NUMBER: O8/952,793
FILING DATE: 1999-DEC-03
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,929
APPLICATION NUMBER: 08/477,929
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,929
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REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-066-960-288/c
; Sequence 288, Application US/10066960
; Publication No. US20030049644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 288:
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /AGENT INFORMATION:
                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: RNA
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                      Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 288, Application US/10409627
Publication No. US20040043923A1
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS
NUMBER OF SEQUENCES: 390
                                                                                                                                                                                                                                                                                                                  26; Indels
                                                                                                                                              OTHER INFORMATION: All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                       OTHER INFORMATION: All U's are 2'-NH2 uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 B. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
                                                                                                                                                                                                                                                                        24.6%; Score 19.4; DB 6; 31.1%; Pred. No. 5.1e+03; iive 16; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/952,793
FILING DATE: 20-NOVEMBER-1997
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/409,627
FILING DATE: 07-Apr-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
                     LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
SEQUENCE CHARACTERISTICS
LENGTH: 97 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                            Best Local Similarity 31.18
Matches 19; Conservative
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US-10-409-627-288/c
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                                                                                                                            FEATURE
                                                                                                                                                                    FEATURE
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90 GTGAGCCTCCTGTCGAATCTTACTACTACTTCTGCTTTGTTTTTGTTTTCCTTGCGTGCCCTT 31
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                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-10-705-300-288/C
US-10-705-300-288, Application US/10705300

Publication No. US20040072234A1

Publication No. US20040072234A1

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS

TITLE OF INVENTION:

TO LECTINS
                                                                                                                                                                                                                                                                                                            Query Match 24.6%; Score 19.4; DB 8; Length 97; Best Local Similarity 31.1%; Pred. No. 5.1e+03; Matches 19; Conservative 16; Mismatches 26; Indels
                                                                                                                                                        OTHER INFORMATION: All C's are 2'-NH2 cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 80111
COMDUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
                                                                                                                                                                   )

OTHER INFORMATION: All U's are 2'-NH2 uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 288:
US-10-409-627-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 B. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/08/952,793
APPLICATION NUMBER: US/08/952,793
FILING DATE: 20.NOV-1997
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05.JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07.JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07.JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07.JUNE-1995
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REFERENCE/DOCKET NUMBER: NEX40C/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/705,300
FILING DATE: 10-Nov-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Barry J. Swanson
LENGTH: 97 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 97 base pairs
                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 288
                                                                            TOPOLOGY: linear
                                                                                                  MOLECULE TYPE: RNA
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Gaps

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4 GGGCGGGGGAGAGGAGCGGCCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCU 62
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| APPLICANT: WILTTEN, Jeffrey P. |
| APPLICANT: SCHWAEBE, Michael |
| APPLICANT: MORAN, Terence |
| TITLE OF INVENTION: WEBSTITUTED QUINOBENZOXAZINE AND |
| TITLE OF INVENTION: METONS OF USING THEREOF |
| FILE REFERENCE: 532232001121 |
| CURRENT FILING DATE: 2006-04-15 |
| PRIOR PLICATION NUMBER: US 10/903,975 |
| PRIOR PLICATION NUMBER: US 10/903,975 |
| PRIOR FILING DATE: 2004-07-30 |
| PRIOR FILING DATE: 2004-07-03 |
| PRIOR PLICATION NUMBER: US 60/461,271 |
| PRIOR PLICATION NUMBER: US 60/463,171 |
| PRIOR PLICATION NUMBER: US 60/519,535 |
| PRIOR FILING DATE: 2003-04-15 |
| PRIOR FILING DATE: 2003-04-15 |
| PRIOR FILING DATE: 2003-04-15 |
| PRIOR PLICATION NUMBER: US 60/519,535 |
| PRIOR PLICATION NUMBER: US 60/532,727 |
| PRIOR PRIOR DATE: 2003-11-12 |
| PRIOR PRIOR DATE: 2003-11-23 |
| NUMBER OF SEQ ION WINDOWS VETSION 4.0 |
| SEQUENCE: 2003-12-23 |
| PRIOR PLICATION NUMBER: US 60/532,727 |
| PRIOR PRIOR DATE: 2003-12-23 |
| PRIOR DATE: 2003-11-2-23 |
| PRIOR PRIOR DATE: 2003-12-23 |
| PRIOR PRIOR DATE: 2003-13-2-23 |
| PRIOR PRIOR DATE: 2003-13-2-23 |
| PRIOR DATE: 2003-21-2-23 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Clone ID: 23-LIB2809-008-Q1-E1-F3 US-09-983-965-1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.3%; Score 19.2; DB 3; 37.5%; Pred. No. 5.9e+03; Live 12; Mismatches 13;
         MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITITE FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
NUMBER: OF SEQ ID NOS: 5912
LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/11106909 Publication No. US20060029950A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 22, Application US/11228636
; Publication No. US20060074089A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.3*
Best Local Similarity 37.5*
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-11-228-636-22
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Patent No. US20020137160A1
GENERAL INFORMATION:
APPLICANT: Tao, Nengbing
APPLICANT: Byatt., John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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; Sequence 6, Application US/10448250
; Sequence 6, Application No. US20040018530A1
; GENERAL INFORMATION:
    APPLICANT: Bowser, Michael T
    APPLICANT: Mendonas, Shaun D
    TILE OF INVENTION: IN VITRO EVOLUTION OF FUNCTIONAL RNA AND DNA USING
    TILE OF INVENTION: IN VITRO EVOLUTION OF FUNCTIONAL
    FILE REPERENCE: 110.01870101
    CURRENT APPLICATION NUMBER: US/10/448,250
    CURRENT FILING DATE: 2003-05-29
    PRIOR APPLICATION NUMBER: 60/384,709
    PRIOR FILING DATE: 2003-05-15
    NUMBER OF SEQ ID NOS: 127
    SOFTWARE: Patentin version 3.2
    SEQ ID NO 6
    LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GAGCGGCUCUGGCCCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 GTGAGCCTCCTGTCGAATCTTACTACTTTGTGTTTTTGTTTTCTTTGCGTGCCCTT 31
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                           Query Match 24.6%; Score 19.4; DB 8; Length 97; Best Local Similarity 31.1%; Pred. No. 5.1e+03; Matches 19; Conservative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.3%; Score 19.2; DB 8; Length 80; 35.9%; Pred. No. 5.9e+03; ive 13; Mismatches 28; Indels
                                                                                                                                                                   All C's are 2'-NH2 cytosine
                                                                                                                                                                                OTHER INFORMATION: All U's are 2'-NH2 uracil SEQUENCE DESCRIPTION: SEQ ID NO: 288:
         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.9%
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: aptamer US-10-448-250-6
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US-09-983-965-1387
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                                                                                                                                      FEATURE
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Sequence 15, Application US/09918740
Publication No. US20030033626A1
GENERAL INFORMATION:
APPLICANT: Hahn, Frederick
APPLICANT: Hahn, Radiheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways to TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XC1
CURRENT APPLICATION NUMBER: US/09/918,740
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0
            Length 39;
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                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT AFFE: LEBACCHDELINE
COMPUTER: TBM COMPETINE
SOFTWARE: FASESEQ for Windows Version 2.0
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/407,123
FILING DATE: 04-Apr-2003
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-No. US/20030181381A1-1999
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ccagaarccarrcrccrccrccrccrcrcrcrcrcrc 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 ccumaaturguacturcegecucenaturgucucuccutuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.8%; Score 18.8; DB 7;
44.7%; Pred. No. 7.6e+03;
tive 9; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-10-407-123-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.7'
GENERAL INFORMATION:
APPLICANT: Himm
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| Publication No. US20060003322A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Shiler, Kvuzat
| TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: Uses thereof
| TITLE APPLICATION UNMERS: US/10/310,914A
| CURRENT FILING DATE: 2002-12-06
| NUMBER OF SEQ ID NOS: 1388402
| SOFTWARE: Patentin Version 3.3
| SEQ ID NO 37212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.1%; Score 19; DB 16; Length 86;
42.4%; Pred. No. 7.1e+03;
tive 9; Mismatches 25; Indels
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0; Mismatches
                                                                                                                                                                                                 FILE REFERENCE: 53223201020
FILE REFERENCE: 532323001820
CURRENT APPLICATION NUMBER: US/11/228,636
CURRENT APPLICATION NUMBER: US/11/228,636
PRIOR APPLICATION NUMBER: US 11/149,007
PRIOR FILING DATE: 2005-09-16
PRIOR FILING DATE: 2004-09-17
PRIOR FILING DATE: 2004-09-17
PRIOR FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 60/688,986
PRIOR SEQ. ID NOS: 29
NUMBER OF SEQ. ID NOS: 29
                                           PIERRE, Fabrice
REGAN, Collin
SCHWAEBE, Michael
YIANNIKOÜROS, George Petros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGAGGGGGGGGAGAGACGAGC 22
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                                                                                                                                     JUNG, Michael
NAGASAWA, Johnny Y.
CHUA, Peter
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Best Local Similarity 90.9
Matches 20, Conservative
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LENGTH: 86
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Gaps

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; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide containing S. cerevisiae DNA
US-11-053-541-15
                                                                                                                                                               Query Match 23.8%; Score 18.8; DB 13; Length 72; Best Local Similarity 28.3%; Pred. No. 8.2e+03; Matches 13; Conservative 16; Mismatches 17; Indels
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Fublication No. US20050241017A1

GENERAL INFORMATION:
APPLICANT: Hahn, Frederick
APPLICANT: Ruehnle, Adelheid
TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways tritle OF INVENTION: Create novel traits in transgenic organisms
TITLE OF INVENTION: create novel traits in transgenic organisms
FILE REFERENCE: KAS-103XCI
CURRENT APPLICATION NUMBER: US/11/053,541
CURRENT FILING DATE: 2005-02-08
PRIOR FILING DATE: 2001-07-31
PRIOR PLICATION NUMBER: 60/221,703
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
SOFTWARE: Patentin Version 3.0
SOFTWARE: Patentin Version 3.0
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Sequence 15, Application US/10835516

Publication No. US20040194162A1

GENERAL INPORMATION:

APPLICANT: WICHONION: Manipulation of genes of the mevalonate and isoprenoid pathways tritle OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways tritle OF INVENTION: Adelheid

TITLE OF INVENTION: Create novel traits in transgenic organisms

TITLE OF INVENTION: OF 2-103XC1

CURRENT FILING DATE: 2004-04-28

FRIOR PAPLICATION NUMBER: US/09/918,740

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2000-07-31

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 76

SEQ ID NO 15

LENGTH: 72
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    NUMBER OF SEQ ID NOS: 76
SOFWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 72
                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                       Best Local Similarity 28.3%
Matches 13; Conservative
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Matches 13; Conservative
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US-11-053-541-15/c
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US-10-835-516-15/c
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Published Applications NA New:*

1: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US06_NEW_PUB.seq:*

2: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US07_NEW_PUB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US07_NEW_PUB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/PC17_NEW_PUB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10_NEW_PUB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11_NEW_PUB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11_NEW_PUB.seq:*

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3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11_NEW_PUB.seq:*

3: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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403, App
10, Appl
216548,
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5, Appli
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9715, Ap
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Sequence 9, Appli
Sequence 618728,
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1061.937 Million cell updates/sec
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                                                                                                     October 16, 2006, 14:34:29 ; Search time 139 Seconds
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-554-1090
US-10-554-710-648
US-10-554-759-648
US-11-357-615-25
US-11-375-551-85
US-11-374-388-403
US-11-374-388-403
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US-11-348-413-216546
US-11-348-413-216547
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US-11-280-456-20
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US-11-348-413-425880
US-11-348-413-425881
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Maximum Match 100%
Listing first 45 summaries
                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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Maximum DB seq length: 100
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No.
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Sequence 425882, Sequence 425883, Sequence 425884.	Sequence 1066900, Sequence 216549,	Sequence 998589, Sequence 13457, A		Sequence 5433, Ap Sequence 5433, Ap		Sequence 49, Appl	Sequence 32, Appl	Sequence 194, App	Seguence 511518,	Seguence 546599,	Sequence 638059,	Sequence 1162729,	Sequence 1162730,	Sequence 1162731,	Sequence 1207851,	Sequence 1207852,
US-11-348-413-425882 US-11-348-413-425883 US-11-348-413-425884	44	US-11-348-413-998589 US-11-292-078-13457	-	US-11-434-184-5433 US-11-434-199-5433	US-11-434-203-5433	US-11-213-668-49	US-11-213-668-32	US-11-043-824-194	US-11-348-413-511518	US-11-348-413-546599	US-11-348-413-638059	US-11-348-413-1162729	US-11-348-413-1162730	US-11-348-413-1162731	US-11-348-413-1207851	US-11-348-413-1207852
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16.2 20.5 16.2 20.5	~ ~ ~	16 20.3		16 20.3 16 20.3		15.8 20.0	8	8	15.6 19.7	9	15.6 19.7	9	1 9	15.6 19.7	6 1	15.6 19.7
2 2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	c 28	c 29	c 31	0 0 33 33	C 34	35	36	c 37	38	c 39	40	41	42	43	n 44	c 45

ALIGNMENTS

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APPLICANT: Jukka T. SALONEN et al:
TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTION
FILE REFERENCE: 0933-0245-DUS1
CURRENT APPLICATION NUMBER: US/11/143,642
CURRENT FILING DATE: 2005-06-03
NUMBER OF SEQ ID NOS: 2039
SOFTWARE: Patentin version 3.3
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                                                                                                                                                               APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: ASHIKARI, TOMOKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR PELING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 173876
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39.4%; Pred. No. 2e+03;
ive 11; Mismatches 9;
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                 Sequence 173876, Application US/11217529
Publication No. US20060099612A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1090, Application US/11143642 Publication No. US20060099610A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Saccharomyces pastorianus
                                                Publication in Application:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHISA
APPLICANT: KODAMA, YUKIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 39.4
Matches 13; Conservative
-11-217-529-173876
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US-11-143-642-1090
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425881,

Sequence

Sequence

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22.5%; Score 17.8; DB 6; Length 9 35.6%; Pred. No. 3.98+03; ive 12; Mismatches 17; Indels
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Sequence 9, Application US/10526765

Publication No. US20060121049A1

GENERAL INFORMATION:
                                    ch 23.0%;
.1 Similarity 48.4%;
15; Conservative 6
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 37.88 Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.59
Best Local Similarity 35.69
Matches 16; Conservative
                                      Query Match
Best Local Similarity
Matches 15; Conserv
US-10-554-759-648
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Sequence 648, Application US/10554759

Publication No. US20060177825A1

Publication No. US20060177825A1

PUBLICANT: University of Georgia Research Foundation

APPLICANT: University of Georgia Research Foundation

APPLICANT: University of Georgia Research Foundation

TITLE OF INVENTION: Global Analysis of Transposable Elements

TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem

TITLE OF INVENTION: cells

FILE REFERENCE: 21099.0077P1

CURRENT APPLICATION NUMBER: US/10/554,759

CURRENT FILING DATE: 2005-10-28

PRIOR APPLICATION NUMBER: 60/466,801

PRIOR FILING DATE: 2003-04-29

NUMBER OF SEQ ID NOS: 770

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:/note = OTHER INFORMATION: Synthetic Construct
                                                                                                                 Query Match 23.3%; Score 18.4; DB 8; Length 51; Best Local Similarity 41.3%; Pred. No. 2e+03; Matches 19; Conservative 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 50;
                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:/note OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                32 CCCUUAAUUGUACUUCGGGCUCGUAUUGUCUCCCUUUCGCCACCU 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.2; DB 6;
Pred. No. 2.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
23.0%;
Best Local Similarity 48.4%;
Matches 15; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                      TYPE: DNA
ORGANISM: Homo sapiens
US-11-143-642-1090
                                                                                                                                                                                                                                                                                              RESULT 3
US-10-554-711-648
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SEQ ID NO 1090
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LENGTH: 50
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LENGTH: 50
                  LENGTH: 51
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TITLE OF INVENTION: CHIMERIC RECOMBINANT PROTEIN AND IN VITRO DIAGNOSIS
FILE REPERRENCE: 122802
CURRENT APPLICATION NUMBER: US/10/526,765
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: PCT/FR03/02712
PRIOR APPLICATION NUMBER: PC1/FR03/02712
PRIOR APPLICATION NUMBER: PC2/11485
PRIOR PILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
SEQ ID NO 9
LENGTH: 90
                                                    Gaps
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US-11-157-615-25

Sequence 25, Application US/11357615

Sequence 25, Application US/11357615

Publication No. US20060188972A1

GENERAL INFORMATION:

APPLICANT: WOLFFE, Alan P.

TILLE OF INVENTION: TARGETED MODIFICATION OF CHROMATIN STRUCTURE

FILE REFERENCE: 8325-0014 / S14-US1

CURRENT APPLICATION NUMBER: US/09/844,508

PRIOR PELLING DATE: 2006-02-16

PRIOR PELLING DATE: 2000-04-28

PRIOR PELLING DATE: 2000-04-28

PRIOR PELLING DATE: 2000-04-28

PRIOR FILING DATE: 2000-08-28

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PATENTING DATE: 2000-08-28

SOFTWARE: PATENTING DATE: 2000-08-28

SOFTWARE: PATENTING DATE: 2000-08-28

SEQ ID NO 25

LENGTH: 77
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  Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: encoding DGGGS linker, 3' to 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TGTAGTTTTGGGTGGTCTTGTTCTTTCTGCCGCCACC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 UGUACUUCGGCUCGUAUUGUCUCCUUUCGCCACC 76
Score 18.2; DB 6;
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.5%; Score 17.8; DB 7; 37.8%; Pred. No. 3.8e+03; trive 11; Mismatches 12;
                                                                                                                                 12 TIGGGACTCGACTGGCTCTCCTTGCTCCTC 42
                                                                                                    45 UNCEGECUCEUAUUGUCUCCUUUCGCCAC 75
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                                                  8; Mismatches
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Gaps

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Gaps
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                                                                  FEATURE: OTHER INFORMATION: Reverse primer sequence used to amplify XptBl
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APPLICANT: Magner, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Scrist, Heather
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 21012.1.5476
CURRENT APPLICATION NUMBER: US 10/099,926
FURENT APPLICATION NUMBER: US 10/099,926
FRIOR FILING DATE: 2002-03-14
FRIOR FILING DATE: 2001-12-26
FRIOR FILING DATE: 2001-12-26
FRIOR FILING DATE: 2001-03-38
FRIOR FILING DATE: 2001-03-38
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-39
FRIOR FILING DATE: 2001-06-38
FRIOR FILING DATE: 2001-06-38
FRIOR FILING DATE: 2001-06-38
FRIOR FILING DATE: 2001-03-38
FRIOR FILING DATE: 2001-08-03
FRIOR FILING DATE: 2000-08-03
FRIOR FIL
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Sequence 10, Application US/10531545
Sequence 10, Application No. USCO060183106A1
GENERAL INFORMATION:
TITLE OF INVENTION: PROCESSES FOR IDENTIFYING
TITLE OF INVENTION: QUADRUPLEX-TARGETED ANTIVIRAL MOLECULES
FILE REFERENCE: 532232000900
CURRENT APPLICATION NUMBER: US/10/531,545
                                                                                                                                                                                                Query Match 21.8%; Score 17.2; DB 9; Length 66; Best Local Similarity 36.8%; Pred. No. 6e+03; Matches 14; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 76;
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                                                                                                                                                                                                                                                                                                                                                                               1 GCTCGAGCAGATTAATTATGCTTCGGATTCATTATGAC 38
                                                                                                                                                                                                                                                                                                                                            24 GCUCUGGCCCCUUAAUUGUACUUCGGCCUCGUAUUGUC 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGANATGNCGAGCTNCTCTGGCATCTNNATGG 35
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NAME/KEY: misc_feature

CCATION: 7, 11, 18, 30, 31, 46, 47, 61, 18, OTHER INFORMATION: n = A,T,C or G

US-11-374-388-403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 403, Application US/11374388
Publication No. US20060193870A1
GENERAL INFORMATION:
TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-374-388-403
                                                                                                                                        US-11-375-551-85
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mounte, William M
APPLICANT: Mounte, William M
APPLICANT: Mounte, Stephen
APPLICANT: Onseted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/USOS/035471
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER: US 60/615,573
NUMBER: OF SEQ ID NOS: 1276209
SEQ ID NO 618728
LENGTH: 25
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CURRENT APPLICATION NUMBER: US/10/753,901
PRIOR APPLICATION NUMBER: US 60/441,717
PRIOR APPLICATION NUMBER: US 60/441,717
PRIOR APPLICATION NUMBER: US 60/441,717
PRIOR PILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.3
SEQ ID NO 85
LENGTH: 66
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; NAME/KEY: misc_feature

; LOCATION: (1)..(25)

; OTHER INFORMATION: SEQ ID NO: 370; WANOIUJA4-5_at; Start 75; Stop 99;

; OTHER INFORMATION: 011101100000000

US-11-348-413-618728
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                               35 UUAAUUGUACUUCGGGCUCGUAUUGUCUCUCCUUUCGCCACCUCC 79 :: |: |: |: |: || || || || || 45 TITAIATAATTCACTTCTCCAATTGTCCCTCATATCTCCTCCTCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.9%; Prec. ....
Watches 9; Conservative 10; Mismatches
                                                                                                                                                                                                                                                            Sequence 618728, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
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APPLICANT: Mitchell, Jon
APPLICANT: Larrinua, Ignacio
APPLICANT: Apel-Birkhold, Patricia
APPLICANT: Schafer, Barry
APPLICANT: Bevan, Scott
APPLICANT: Young, Scott
APPLICANT: Guo, Lining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 GGTCGTATTTCTCTCATTTCG 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: probe
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ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                             RESULT 7
US-11-348-413-618728/C
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Gaps
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                                        APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high
FILE OF INVENTION: density...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele

: LOCATION: 24

: LOCATION: 24

: CTHER INFORMATION: 99-2832-152 : polymorphic base C or

US-11-370-584-3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/11243296A

Sequence 5, Application US/11243296A

Publication No. US20060112443A1

GENERAL INFORMATION:

APPLICANT: Van der Linden, C.G.

APPLICANT: Smulders, J.M.

APPLICANT: Smulders, J.M.

APPLICANT: Choo, Cheah B-type gene from oil palm

ITILE OF INVENTION: Novel B-type gene from oil palm

FILE REFERENCE: SHDEL2.002AUS

CURRENT APPLICATION NUMBER: US/11/243,296A

CURRENT FILING DATE: 2005-09-30

PRIOR APPLICATION NUMBER: MY PI 20044004

PRIOR APPLICATION NUMBER: WY PI 20044004

SPRIOR APPLICATION NUMBER: WY PI 20044004

NUMBER OF SEQ ID NOS: 26

SEQ ID NO S.

SEQ ID NO S.
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                                                                                                                                                                        FILE KEFEKEREL CATTON NUMBER: US/11/370,584
CURRENT FILING DATE: 2006-03-08
PRIOR APPLICATION NUMBER: US/10/349,143
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2003-01-21
PRIOR PLING DATE: 1999-10-20
PRIOR PLING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: US 09/298,850
PRIOR APPLICATION NUMBER: US 60/109,732
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PLING DATE: 1998-11-23
PRIOR PILING DATE: 1998-11-23
PRIOR PILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 3264

LENGTH: 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.5%;
89.5%;
  Publication No. US20060177863A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Elaeis guineensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conserv
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APPLICANT: Mounts, william M
APPLICANT: Mounts, william M
APPLICANT: Murphy, Ellen
APPLICANT: Olmeted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/USO5/035471
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NOS: 1276209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GGAGGGGGGGGGGGGGGAAGGTTAGCGACACGCAATTGCTATAGTGAGTCGTATTAG 78
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21.8%; Score 17.2; DB 6; Length 99;
Best Local Similarity 40.3%; Pred. No. 6.8e+03;
Matches 25; Conservative 9; Mismatches 28; Indels
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CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: PCT/US03/33366
PRIOR FILING DATE: 2003-10-20
PRIOR PRIOR APPLICATION NUMBER: US 60/419,456
PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 99
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US-11-370-584-3264/c
; Sequence 3264, Application US/11370584
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Best Local Similarity 36.0%,
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OTHER INFORMATION: probe
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
ITILE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-008-100 (AM 101724)
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR PLILING DATE: 2005-10-05
PRIOR PLILING DATE: 2005-10-05
PRIOR PLILING DATE: 2004-10-05
SPIOR FILING DATE: 2004-10-05
SEQ ID NO 216546
LENGTH: 25
LENGTH: 25
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Oldsted, Stephen
TTLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
TTLE OF INVENTION: DATE: 2006-08-4100 (AM 101724)
CURRENT APPLICATION NUMBER: DS/11/348,413
CURRENT FILING DATE: 2005-00-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
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; NAME/KEX: misc feature

; LOCATION: (1)...(25)

; OTHER INFORMATION: SEQ ID NO: 6358; WANOIUKNQ; Start 1513; Stop 1537;

; OTHER INFORMATION: 000000011100000

US-11-348-413-216546
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. OTHER INFORMATION: SEQ ID NO: 6358; WANDIUKNQ; Start 1514; Stop 1538;
. OTHER INFORMATION: 000000011100000
US-11-348-413-216547
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21.0%; Score 16.6; DB 9; Length 25;
Best Local Similarity 39.1%; Pred. No. 7.5e+03;
Matches 9; Conservative 10; Mismatches 4; Indels
Sequence 216546, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
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Publication No. US20060160121A1
GENERAL INFORMATION:
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OTHER INFORMATION: probe
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LOCATION: (1)..(25)
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LENGTH: 25
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   Length 25;
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Query Match
21.0%; Score 16.6; DB 9;
Best Local Similarity 39.1%; Pred. No. 7.5e+03;
Matches 9; Conservative 10; Mismatches 4;
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Search completed: October 16, 2006, 14:51:29 Job time : 140 secs

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October 16, 2006, 13:53:09 ; Search time 125.594 Seconds (without alignments) 1332.341 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Add94592 Murine IF Adx5646 HIV-1 pro Aef13105 Human mut Adc05103 Human Na/ Adc05103 Human Na/ Adc05106 Human Na/ Adc05106 Human Na/ Adc05106 Human Na/ Adc05107 Human Na/ Add78850 Sequence Aqq4882 Oligonucl Aq4882 Oligonucl Aq4882 Oligonucl Aq4882 Oligonucl Aq4882 Oligonucl Adx93772 Nucleotid Aav31727 Nucleotid Aav31727 Nucleotid Aav36011 Oligonucl Acc26021 Human all Acc28837 Human all Acc27983 VIC/FI-I Ada05553 Murine ET Adc0553 Human all Acx1963 Human adi Adx04519 Human adi Adx04519 Human adi Adx04519 Human adi Adx04519 Human adi	INTS	PGR exon ORF15 repetitive sequence. GrPase regulator; RPGR; genotyping; initis pigmentosa; XLRP; lysis; ds.	sposition to disease, associated with disease tis pigmentosa GTPase regulator gene by e, and determining presence of mutations. English. associated with a disease causing mutations associated with a disease causing mutations determining whether the genotype comprises a where the risk genotype is present within open
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Indels Length

Score 15.6; DB 2; Pred. No. 4.5e+03; 7; Mismatches 4;

65.0**%**; 50.0**%**;

11; Conservative

Query Match Best Local Similarity Matches 11; Conserv

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23 TTTTCTCCCTCCACCACCTC 2

BP

AAQ44806 standard; DNA; 24

RESULT 3 AAQ44806

24;

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reading frame (ORF)15 of the RPGR gene. The method is useful for detecting a certain disease state e.g., X-linked retinitis pigmentosa (XLRP). The kit is useful for detecting and measuring disease causing mutations in biological fluids and tissues and for localising mutation in tissues. The mutant RPGR gene is useful in gene therapy techniques and for screening agents capable of affecting the expression of the sequences and/or the biological activity of mutant RPGR. They are preferably useful for identifying agonists and antagonists of RPGR. The mutant RPGR gene is also useful in identification of potential pharmaceutical targets in high throughput screening assays and forensic analysis. The present sequence is the imperfect direct repeat of human RPGR exon ORFIS repetitive DNA
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single-strand binding protein; PUR protein; cellular oncogene; eukaryotic origin of replication; gene amplification; cancer cell; retinoblastoma protein; helix-destabilising protein; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and expression of PUR protein, involved in regulation of replication - also oligo:nucleotide(s) and antibodies for use in treatment of proliferative diseases, e.g. cancer.
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                                                                                                                                                                                                                Match 65.8%; Score 15.8; DB 4; Length 24; Local Similarity 52.6%; Pred. No. 3.7e+03; les 10; Conservative 7; Mismatches 2; Indels
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28-SEP-1994
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Single-strand binding protein; PUR protein; cellular oncogene; eukaryotto origin of replication; gene amplification; cancer cell; retinoblastoma protein; helix-destabilising protein; inhibitor; hyperproliferation; c-myc; ss.

93WO-US008102. 92US-00938189. 93US-00014943.

27-AUG-1993; 28-AUG-1992; 02-FEB-1993;

17-MAR-1994

WO9405689-A1

Synthetic.

Oligonucleotide MR0700 used in characterising c-myc PUR element.

(first entry)

(revised)

25-MAR-2003 28-SEP-1994

AAQ44806;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotides AAQ44802-Q44809 were used in the characterisation of a sequence element found 1.6kb upstream of the cellular c-myc gene. The PUR element (see AAQ44801) is located in a region of DNA bending activity which is a structural feature often associated with origins of DNA replication. The PUR protein AAR50310 binds to the PUR element. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                  Cloning and expression of PUR protein, involved in regulation of DNA replication - also oligo:nucleotide(s) and antibodies for use in the treatment of proliferative diseases, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 4.5e+03; ive 7; Mismatches 4; Indels
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TTTCTCCCTCCACCACCTC 23
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                                                                                                                                                                                                                                                                                                                                     Johnson EM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  axxxb
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PUR elements are purine-rich 24 nucleotide DNA sequences which occur at cuelaryotic origins of replication and 5' flanking regions of some cellular oncogenes. The PUR procesi (ARR50310) was originally identified as a 27kD HeLa cell nuclear factor that bound in a sequence-specific manner to a major site of DNA bending located 1.6kb upstream of the transcription start site of the human c-myc gene; the site recognised by PUR procein had the sequence AAQ44801. (Updated on 25-MAR-2003 to correct

Claim 6; Page 65; 97pp; English

C; 14 G; 2 T; 0 U; 0 Other;

Sequence 24 BP; 8 A; 0

Gaps

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This is the nucleotide sequence of the PUR element used in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins. Inhibitors of PUR activity may be useful for treating viral infections and hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of an oligonucleotide used in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins inhibitors of PUR activity may be useful for treating viral infections
                                                                                                 PUR protein and its fragments - that inhibit PUR protein binding to PUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein and its fragments - that inhibit PUR protein binding to PUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUR-alpha gene; inhibition; viral infection; cancer; PUR element; hyperproliferative disease; ss.
                                                                                                                                                                                                                                                                                                                            Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 4.5e+03; Matches 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.6; DB 2; Length 24; Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                             Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of the oligonucleotide MR0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6.1.1; Col 27; 63pp; English
(MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                   3 UNGUCUCUCCUUUCGCCACCUC 24
                                                                                                                                                      Disclosure, Col 12; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     23 TTTCTCTCCCTCCACCACCTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00470911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV31731 Standard; DNA; 24
                                Johnson EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                       element or other proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    element or other proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-321632/28.
                                                                 WPI; 1998-321632/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bergemann AD,
                                  Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV31731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV31733
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8X1X8X11X8X2X00000X8
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Assays for PUR protein ligands or modulators - using immobilised PUR protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The probes AAT99270-T99277 were used to screen for positive clones containing a 467 bp Sau3AI fragment of the human c-myc upstream region cloned into pUC19. Isolated sequences were then used as probes to screen an expression library for sequences encoding the PUR protein. The PUR sequence can be used to identify chemical or biological compounds that bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may be used to treat hyperproliferative diseases such as cancer
                                               PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss; cancer; probe; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
hyperproliferative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 4.5e+03; Matches 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 2 A; 14 C; 0 G; B T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of the PUR element
                                                                                                                                                                                                                                                                                                                              (MOUN ) MOUNT SINAI SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 uneucuccumoceccaccuc 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TTTCTCTCCCTCCACCACCTC 23
                Human PUR-alpha gene probe MR0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Col 26; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                         93US-00014943.
                                                                                                                                                                                                                         95US-00486421
                                                                                                                                                                                                                                                           92US-00938189
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93US-00014943
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                                                                                                                                                                                                                                                                                                                                                                  Bergemann AD, Johnson EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV31726 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-488859/45.
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                         02-FEB-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1992;
02-FEB-1993;
                                                                                                                                                                                                                                                           28-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36-JUN-1995;
                                                                                                                                                      US5672479-A.
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                                                                                                                                                                                    30-SEP-1997
                                                                                                   Synthetic
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The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. PUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR persent esquence represents an oligonucleotide used in the identification and characterisation of the PUR protein and its sequence element PUR repeat, in an example from the
Oligonucleotide MR0700 used in PUR identification/characterisation
                                            PUR element, PUR-alpha, hyperproliferative disease, cancer, human, monoclonal antibody, identification, characterisation, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody specific for PUR protein - useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromatin; DNA hybridization; DNA amplification; DNA microarray; diagnosis; ss; primer; PCR; OLIG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3' primer for PCR of DNase I treated OLIG2 chromatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 2 A; 14 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.0%; Score 15.6; DB 2; Best Local Similarity 50.0%; Pred. No. 4.5e+03; Matches 11; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                          SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITICICICCICCACCACCTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ungueneceumoceceaecue 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Col 27; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                         95US-00486809.
                                                                                                                                                                                                                                                                                                                     92US-00938189
                                                                                                                                                                                                                                                                                                                                        93US-00014943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEE94315 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-152881/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2005118873-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bergemann AD,
                                                                                                                                                                                                                                                                                                                                                                                                            TWUOM ( NUOM)
                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-2006
                                                                                                                                                                                                                                                                                                                                             02-FEB-1993;
                                                                                                                                                                                US5869622-A.
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                                                                                                                                                                                                                              09-FEB-1999
                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. FUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR gene. The present sequence represents an oligonucleotide used in the identification and characterisation of the PUR protein and its sequence element PUR repeat, in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
       Gaps
                                                                                                                                                                                                                                                                                                                                             Oligonucleotide MF0677 used in PUR identification/characterisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody specific for PUR protein - useful for treating
                                                                                                                                                                                                                                                                                                                                                                                       PUR element, PUR-alpha, hyperproliferative disease, cancer; human, monoclonal antibody; identification; characterisation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 4.5e+03;
7; Mismatches 4; Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 8 A; 0 C; 14 G; 2 T; 0 U; 0 Other;
         4
       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SINAI SCHOOL MEDICINE.
                                                 3 UNGUCUCUCCUUUCGCCACCUC 24
                                                                           rrrcrcccrccaccacc 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 UNGUCUCUCCUUUCGCCACCUC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Col 27; 64pp; English.
                                                                                                                                                                                                            BP
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00486809
                                                                                                                                                                                                         AAX04070 standard; DNA; 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergemann AD, Johnson EM;
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-152881/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNUOM ( NUOM)
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02-FEB-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                12-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5869622-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                        AAX04070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
       Matches
                                                                                                                                                                                    AAXO4070/C
XX
AAX
AAXO,
XX
AAXO,
XX
AAXO,
XX
AAXO,
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AAXO,
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BO D119G
XX
BO 
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AAX04075
ID AAX0
XX
AC AAXC
XX
XX
YX
DT 12-P

RESULT 8

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Gaps

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Length 24; 4; Indels

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The Hew Invention relates to detecting open chromatin in genomic DNA by determining the hybridization of acapture probe to a treated sample amplification products and the untreated sample amplification products and the untreated sample amplification products.

CC Specifically, the method comprises preparing a chromatin sample with an open chromatin DNA cleaving agent or produce the chromatin sample with an open chromatin DNA cleaving agent to produce fragments performing a first amplification reaction using the fragments as a substrate, to produce treated-sample amplification products; concerning a second amplification reaction using the fragments as a substrate, to produce treated-sample amplification products and the chromatin DNA cleaving agent, to produce untreated-sample amplification products and the chromatin DNA cleaving agent, to produce untreated-sample amplification products with a capture probe; and cerraming the hybridization of the capture probe; and determining the hybridization of the capture probe to the products ample amplification products with a capture probe to the capture amplification products seem the presence of open chromatin in the genomic DNA. Also given treated-sample amplification products as compared to the hybridization of the capture probe to the untreated-sample amplification products as compared to the hybridization of the capture probe to the untreated sample amplification products as compared to the hybridization of the capture probe to the untreated sample amplification products as compared to the hybridization of creatment in genomic DNA. The methods and chromatin state profiling array, for detecting the presence of open chromatin in genomic DNA, used in chromatin state profiling array, for detecting the response of cells and patients to candidate or reatment and evaluating the response of cells and patients to confidence or primer for one-sided PCR amplification of PNAse I treatment and evaluating profiling array.

Creatment and evaluating the response of DNAse I treatmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic DNA by
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                                                                                                                                                                                                                                   Detecting open chromatin comprises determining hybridization of the capture probe to the treated- and untreated-sample amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to detecting open chromatin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine IFN-gamma associated probe SEQ ID 2144.
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                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 37; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ATTCTCTCTTTTTCTCCTCT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The new invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                      WPI; 2006-047578/05
(CEMI-) CEMINES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-2004
                                                                             Neuman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI94591;
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AD194591/C
ID AD194591/C
XX
AC AD194
XX
DT 04-NO
XX
KW funct:
KW detect
KW human
XX
NX
KW RECCO
XX
KW COOO
XX
COS MUS W
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EN WO200
XX
EN WO
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                               functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; ss; probe.
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24-MAY-2001; 2001WO-US017086.

WO200190337-A2

29-NOV-2001

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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered tunctionality in a nucleic acid cleavage assay. The enzyme comprises a 5, conclease, preferably a thermostable 5, nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a copymerase such that it exhibits reduced DNA synthetic activity from that comprises to fit he naturally occurring polymerase. Preferably the polymerase is a thermostable polymerase from a Thermus species such as T. aquaticus, T. Clarvage assay and an animo acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved cleavage assay and an amino acid sequence that provides inproved cleavage assay and an amino acid sequence that provides inproved cleavage assay and an amino acid sequence that provides inproved cleavage assay and an amino acid sequence that provides inproved cleavage assay and an amino acid sequence that provides inproved cleavage structure comprises a RNA target nucleic acid (a cytochrome cleavage structure comprises a RNA target nucleic acid (a cytochrome comprises an non-target cleavage of the invasive cleavage structure comprises of fluorescence energy transfer or by detecting radioctivity luminescence, which is then detected by captering radioctivity luminescence, which is then detected by comprising and octivity the nucleic acid (a cell lysate) comprising substrate concleavage product. The enzyme is employed for detecting target DNAs and cleavage product. The enzyme is employed for detecting target DNAs and concleavage product. The enzyme is employed for detecting target DNAs and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with for cheavage product in a parameter and mutant alleles of genes including genes and the parameter and the parameter and mutant alleles of genes including genes and concerne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease or other conditions. In addition, the enzymes may be useful for detecting and identifying strains of microorganisms including bacteria, fungi, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
                                                                                                                                                                                                                                V, Ma W;
Takova TY;
                                                                                                                                                                                             Hall JG;
V, Ma W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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ski RW, Lukowiak AA, Lyamichev
Schaefer JJ, Skrzypczynski Z,
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63.3%; Score 15.2; DB 7; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.6e+03;
Matches 10; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 9 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 95; SEQ ID NO 2144; 1266pp; English.
                                                                                                                                                       (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                               1, Bartholomay CT, Chehak
Kaiser M, Kwiatkowski RW,
Inoz MC, Olson SM, Schaefe
                                                                                                                                                                                                                                                                                 Lyamichev NE, Neri BP;
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                                             11-JAN-2001; 2001US-00758282.
24-MAY-2001; 2001US-00864426.
24-MAY-2001; 2001US-00864636.
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ID ADI94589 standard; DNA; 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                       WPI; 2002-083110/11.
                                                                                                                                                                                                                                   Ip HS, Kaiser M
Olson-Munoz MC,
                                                                                                                                                                                                                                                                                      Vedvik KL,
                                                                                                                                                                                                        Allawi H,
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RXXXXXXXX
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functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; 88; probe.

Murine IFN-gamma associated probe SEQ ID 2143.

(first entry)

04-NOV-2004

ADI94590;

ВЪ

ADI94590 standard; DNA; 27

ADI94590

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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered to contains a heterologous functional domain that provides altered to contains a heterologous functional domain that provides altered to a nuclease, preferably a thermostable 5' nuclease, or a polymerase which is altered in sequence related to a naturally occurring sequence of a polymerase such that it exhibits reduced DNA synthetic activity from that of thermostable polymerase from a Thermus species such as T. aquaticus, T. flavus, T. thermophilus, T. filiformus or T. scotoductus. The enzyme comprises a hereologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage assay and an amino acid sequence that provides improved cleavage seasy and an amino acid sequence that provides improved cleavage structure comprises a RNA target nucleic acid (a cytochrome P550, or cytokine RNA). Cleavage of the invasive cleavage structure comprises a non-target cleavage product, which is then detected by detecting radioactivity luminescence, phosphorescence, fluorescence of polarisation or charge. The enzyme is useful for cleaving a uncleic acid to the enzyme which produces at least one detectable nucleic acid to the enzyme which produces at least one detectable cleavage product. The enzyme is employed for detecting target DNAs and RNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with disease or other conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
functional domain; nucleic acid cleavage assay; nuclease; polymerase;
detection; microorganism; RNA genome; hepatitis C;
human immunodeficiency virus; ss; probe.
                                                                                                                                                                                                                                                                                                                                                                                                  H, Bartholomay CT, Chehak L, Curtis ML, Eis PS,
Kaiser M, Kwiatkowski RW, Lukowiak AA, Lyamichev
Unoz MC, Olson SM, Schaefer JJ, Skrzypczynski Z,
KL, Lyamichev NE, Neri BP;
                                                                                                                                                                                                                                                                                                                                                                                                                               Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 95; SEQ ID NO 2142; 1266pp; English.
                                                                                                                                                                                                                                                                                                                                                                 (THIR-) THIRD WAVE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                             11-JAN-2001; 2001US-00758282.
24-MAY-2001; 2001US-0086426.
24-MAY-2001; 2001US-00864636.
                                                                                                                                                                                                                 24-MAY-2001; 2001WO-US017086
                                                                                                                                                                                                                                                           2000US-00577304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Olson-Munoz MC,
                                                                                                                                WO200190337-A2
                                                                                        Mus musculus
                                                                                                                                                                                                                                                           24-MAY-2000;
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V, Ma W; Takova TY;

Hall JG;

Curtis ML, Eis PS, towiak AA, Lyamichev

Chehak L, Curtis ML, Eis PS, ski RW, Lukowiak AA, Lyamichev Schaefer JJ, Skrzypczynski Z,

(THIR-) THIRD WAVE TECHNOLOGIES INC.

24-MAY-2000; 2000US-00577304. 11-JAN-2001; 2001US-00758282. 24-MAY-2001; 2001US-00864426. 24-MAY-2001; 2001US-00864636.

24-MAY-2001; 2001WO-US017086.

Takova TY;

V, Ma W;

Hall JG;

WO200190337-A2 Mus musculus.

29-NOV-2001.

ID HS, Kaiser M, Kwiatkowski RW, Olson-Munoz MC, Olson SM, Schaefe Vedvik KL, Lyamichev NE, Neri BP;

WPI; 2002-083110/11.

Bartholomay CT,

Allawi H,

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detecting and identifying strains of microorganisms including bacteria,
                               fungi, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                                                                                    63.3%; Score 15.2; DB 7; Length 22; 50.0%; Pred. No. 6.6e+03; ive 7; Mismatches 3; Indels
                                                                                                                                                                                  Sequence 22 BP; 9 A; 3 C; 9 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Best Local Similarity
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Gaps

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s gucuccuuucgccaccuc 24
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21 Grcrcrrrrgccagrrc 2

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10; Conservative

Matches

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This invention describes a novel composition comprising an enzyme which contains a heterologous functional domain that provides altered according a heterologous functional domain that provides altered contains a heterologous functional domain that provides altered in sequence related to anaturally occurring sequence of a altered in sequence related to anaturally occurring sequence of a copymerase such that it exhibits reduced DNA synthetic activity from that of the maturally occurring polymerase. Preferably the polymerase is a comprises a heterologous functional domain, an amino acid sequence that or thermostable polymerase from a Thermus species such as T. aquaticus, T. flilformus or T. soctoductus. The enzyme comprises a heterologous functional domain, an amino acid sequence that provides an improved substrate binding activity in the nucleic acid cleavage sasay and an amino acid sequence that provides improved cleavage structure comprises a RNA target nucleic acid (a cytochrome packer) or cytokine RNA). Cleavage function cleavage structure comprises a RNA target nucleic acid (a cytochrome packer) or cytokine RNA). Cleavage product, which is then detected by detecting radioactivity luminescence, phosphorescence, fluorescence comprising and nucleic acid to the enzyme which produces at least one detectable cleavage product. The enzyme is useful for cleavage DNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with disease or other conditions. In addition, the enzyme such animal or plants that are or may be associated with indust, protozoa, ciliates and viruses, preferably detecting and human clear animal or plants when a perzyme is neighborescence in an implication or described and viruses, preferably detecting and human clear animal or plants when an enzyme is neighborescence and viruses, preferably detecting and human clear animal or plants has been any be allocating and industrible and viruses, preferably preferably provided an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
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polarisation or charge. The enzyme is useful
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Matches
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V, Ma W;
Takova TY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising enzyme which comprises heterologous functional domain that provides altered functionality in nucleic acid cleavage assay, useful for cleaving nucleic acid, and detecting presence of RNA
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C;
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Lyamichev
                                                                        Score 15.2; DB 7; Length 27;
Pred. No. 6.8e+03;
7; Mismatches 3; Indels
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                            C; 4 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         functional domain; nucleic acid cleavage assay; detection; microorganism; RNA genome; hepatitis human immunodeficiency virus; ss; probe.
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24-MAY-2001; 2001US-00864426.
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                                                                                                             50.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                Best Local Similarity 50.0
Matches 10; Conservative
                            BP; 3 A; 10
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                         Sequence 27
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                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI94588;
                                                                                                                                                                                                                                                                                                                                               RESULT 13
AD194588
1D AD194588
1D AD194588
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target; substrate; catalyst; modulation; expression; Raf gene; delivery;
streening; identification; synthesis; deprotection; purification; cancer;
inflammation; psoriasis; non-hepaic ascites; infection; genetic drift;
restenosis; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.
for cleaving a nucleic acid
             which involves exposing a sample (a cell lysate) comprising substrate nucleic acid to the enzyme which produces at least one detectable cleavage product. The enzyme is employed for detecting target DNAs and RNAs comprising wild-type and mutant alleles of genes including genes from humans, other animal or plants that are or may be associated with disease or other conditions. In addition, the enzymes may be useful for detecting and identifying strains of microorganisms including bacteria, fungl, protozoa, ciliates and viruses, preferably detecting and identifying viruses having RNA genomes, such as hepatitis C and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A method has been developed for the identification of a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bellon L;
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                                                                                                                                                                                                                                                         Match 63.3%; Score 15.2; DB 7; Length 28; Local Similarity 50.0%; Pred. No. 6.8e+03; les 10; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human C-raf hammerhead ribozyme nucleotide position 220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kisich K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K,
Parry T, Beigelman L, Mcswiggen JA, Karpeisky A,
Thompson J, Workman CT, Beaudry A, Sweedler D;
                                                                                                                                                                                                                             Sequence 28 BP; 3 A; 11 C; 4 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beigelman L, Mcswiggen JA, I, Workman CT, Beaudry A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 151; Page 146; 259pp; English.
                                                                                                                                                                                                                                                                                                                                           5 GUCUCCUCUUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                 8 GTCTCTTTTGCCAGTTC 27
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97US-0051718P.
97US-0056808P.
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97US-0061324P.
97US-0064866P.
97US-0068212P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV91451 standard; RNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                       immunodeficiency virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV91451;
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comprises: (a) introducing into the system a random library of nucleic acid catalyste (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalysic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of a least part of the SBDs in such systems. Nucleic acid molecules with endomuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid motecules with are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid motecules with a socites and infection. They may also be used to detect genetic distance ascites and infection. They may also be used to detect genetic drift and muttancions in diseased cells and to determine c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of such they appered to the subscience of sugar/phosphate modifications increases stability against nuclease and activity. AAV90922 to AAV93877 repersent NACs that can be used in the method, specifically for modulating the expression of a Raf gene
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                            61.7%; Score 14.8; DB 2; Length 29; 47.4%; Pred. No. 1e+04; tive 7; Mismatches 3; Indels
Sequence 29 BP; 11 A; 3 C; 9 G; 0 T; 5 U; 1 Other;
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                                                                                                           Local Similarity 47.4%;
tes 9; Conservative
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Gaps

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AAF01081 standard; RNA; 29
                                                                 (first entry)
                                                                                                   Hammerhead ribozyme #1072
                                                                   16-FEB-2001
                                AAF01081;
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ВР

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Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; 88.
                                                                            11-APR-2000; 2000WO-US009721
                                                                                    99US-0129390P
                                                                                           (RIBO-) RIBOZYME PHARM INC.
                                                            WO200061729-A2
                                                    Homo sapiens
                                                                                    12-APR-1999;
                                                                    19-OCT-2000
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Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin. Mcswiggen J; Zwick M, Pavco P, WPI; 2000-647423/62. Blatt L,

Claim 32; Page 80; 164pp; English.

The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATI Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha

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                                 29;
                                                         Indels
                               Score 14.8; DB 3; Length
Pred. No. 1e+04;
          Seguence 29 BP; 13 A; 2 C; 9 G; 0 T; 4 U; 1 Other;
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completed: October 16, 2006, 14:16:00 Search completed: Octobe Job time : 126.594 secs

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Sequence:

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AX649756 Sequence
A24320 LST3 primer
AR010021 Sequence
124749 Sequence 12
BD177162 Method fo
BD177154 Method fo
AX648244 Sequence
BD268715 Inhibitor
CO764854 Sequence
AR229112 Sequence
AR229112 Sequence
AR329112 Sequence
AR31780 Sequence
AR31780 Sequence
AR31780 Sequence
AR5307680 Sequence
AX649749 Sequence
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Johnson, E.M. and Bergemann, A.D.
Cloning and expression of PUR protein
Patent: US 5756684-A 20 26-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                           24 bp
Sequence 20 from patent US 5756684.
AR010008
AR010008.1 GI:3968813
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/organism="unknown"
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Sequence 38 from patent US 5756684.
AR010025.1 GI:3968830
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1 (bases 1 to 24)
Johnson, E.M. and Bergemann, A.D.
                                                           AX648244
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AR314584
AR312823
AR317580
AR337580
AR337580
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AX649749
BD206822
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Matches 11; Conservative
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AUTHORS
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AR014743 Sequence
AR034743 Sequence
AR034760 Sequence
124740 Sequence 3
124752 Sequence 15
BD55319 Regulatio
AR265215 Sequence
AR072296 Sequence
126407 Sequence 38
IS847 Sequence 38
AX649751 Sequence
AX649752 Sequence
                                                          Search time 590.797 Seconds (without alignments) 2597.742 Million cell updates/sec
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AX649754 Sequence
AX649755 Sequence
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          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                          1796954
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                                                                                                               uauugucucuccuuucgccaccuc 24
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Maximum Match 100%
Listing first 45 summaries
                                            model
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AR010025
AR034743
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AR265215
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seq length: 30
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Minimum DB Maximum DB

Database

Searched:

PAT 04-DEC-1998

PAT 04-DEC-1998

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No.

Result

PAT 07-0CT-1996

linear

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24 bp
Sequence 3 from patent US 5545551.
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2 TITICICTCCCTCCACCACCTC 23
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JP 2002541795-A/1072.
unidentified
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124740.1 GI:1604610
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nes 11; Conservative
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                            RESULT 5
124740/c
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124752
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                                                                                                     65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 1.9e+04;
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                                                                                                                                4; Indels
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                                                                                                                                                                                                                                                                                                                                     Unclassified.

1 (bases 1 to 24)

2 (bases 1 to 24)

Monoclonal antibodies to the pur protein

Patent: US 5869622-A 20 09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 24)
Johnson, E.M. and Bergemann, A.D.
Monoclonal antibodies to the pur protein
Patent: US 5869622-A 38 09-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.0%; Score 15.6; DB 2; 50.0%; Pred. No. 1.9e+04;
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                                                                                                                                                                                                                                                  DNA
and expression of PUR protein US 575684-A 38 26-MAY-1998, Location/Qualifiers
                                                                                                                             7; Mismatches
                                                    /organism="unknown"
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    .24
    /organism="unknown"
    /mol_type="unassigned DNA"

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Seguence 20 from patent US 5869622.
AR034743
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Matches 11; Conservative
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  Cloning and
Patent: US 5
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Matches 11; Conserv
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                                                                                                        Query Match
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AR034743/c
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buzsazyy 29 bp RNA linear PAT 17-JUL-2003
Regulation of repressor genes using nucleic acid molecules.
BD253279
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unclassified sequences.
1 (bases 1 to 2 avick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
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50.0%; Pred. No. 1.9e+04;
tive 7; Mismatches 4;
1 (bases 1 to 24)
Johnson, E.M. and Bergmann, A.D.
Cloning and expression of pur protein
Patent: US 5545551-A 3 13-AUG-1996;
Location/Qualifiers
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1 (bases 1 to 24)
Johnson, E.M. and Bergmann, A.D.
Cloning and expression of pur protein
Patent: US 554551-A 15 13-AUG-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 from patent US 5545551.
124752
124752.1 GI:1604622
                                                                                                          1. .24
/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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1. .21
/organism="unknown"
/mol_type="unassigned DNA"
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                                        DESCRIPTION OF THE PROPERTY OF
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Location/Qualifiers
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Sucov, H.M., Evans, R.M. and Umesono, K.
Response element compositions and assays employing same Patent: US 6492137-A 16 10-DEC-2002;
The Salk Institute for Biological Studies; La Jolla, CA Location/Qualifiers
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Location/Qualifiers
Patent: JP 2002541795-A 1072 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
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Sequence 99 from patent US 5948611.
AR072296.1 GI:9999060
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Sequence 16 from patent US 6492137.
AR265215.1 GI:29693642
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/mol_type="genomic RNA"
/db_xref="taxon:32644"
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(C12N5/00,C12R1:91)
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Matches 9; Conservative
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C12R1:91),
PC (C12P2)
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1 (bases 1 to 18)

Prockop, D. J., Ala-Kokko, L., Williams, C. J., Ritvaniemi, P.,

Baldwin, C., Hopkinson, I. and Ahmad, N. Nina.

Primers and methods for detecting mutations in the procollagen II

gene (COL2A1) that indicate a genetic predisposition for a

COL2A1-associated disease

Patent: US 5948611-A 99 07-SEP-1999;

Location/Qualifiers
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Prockop, D.J., Ala-Kokko, L. and Ritvaniemi, P.
Primers and methods for detecting mutations in the procollagen II
gene that indicate a genetic predisposition for osteoarthritis
Patent: US 5558988-A 99 24-SEP-1996;
Location/Qualifiers
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62.5%; Pred. No. 6.5e+04;
iive 5; Mismatches 1;
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62.5%; Pred. No. 6.5e+04;
ive 5; Mismatches 1;
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1 (bases 1 to 21)
Watanabe, K. B., Ren, W.-Y. and Weil,R.
Complementary DNA and toxins
Patent: US 5571937-A 38 05-NOV-1996;
Location/Qualifiers
                                                                                                                                                                                 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 99 from patent US 5558988.
126407
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/mol_type="unassigned DNA"
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Sequence 38 from patent US 5571937.
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Best Local Similarity 52.6
Matches 10; Conservative
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Matches 10; Conserva
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                          59.2%; Score 14.2; DB 2; Length 21; 36.8%; Pred. No. 8.1e+04;
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Patent: EP 1273660-A 1590 08-JAN-2003;
Aeomica, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.2%; Score 14.2; DB 2; Best Local Similarity 36.8%; Pred. No. 8.1e+04; Matches 7; Conservative 9; Mismatches 3;
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52.6%; Pred. No. 8.2e+04;
:ive 6; Mismatches 3;
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Sequence 1590 from Patent EP1273660.
AX649750. GI:29152568
                                                    9; Mismatches
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Sequence 38 from patent US 5652350.
158747 GI:2477985
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                                      Best Local Similarity 36.8
Matches 7; Conservative
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Best Local Similarity 52.6
Matches 10; Conservative
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                                                                                                                                                                                                                                            Unknown.
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                           Query Match
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AX649750/c
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Patent: EP 1273660-A 1591 08-JAN-2003;
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Patent: BP 1273660-A 1592 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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52.6%; Pred. No. 8.2e+04;
tive 6; Mismatches 3;
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Sequence 1591 from Patent BP1273660.
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Sequence 1592 from Patent EP1273660.
AX649752
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    /mol_type="unassigned DNA"
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Location/Qualifiers
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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SUMMARIES

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ΩI	AZ775852	BQ586604	AI673609	CL983097	AZ604126	CA850924	AZ340258	AZ329650	AZ514958	CL983109	BH901484	DME545811	AZ475883	AI539240	AZ454352	AI183010	AZ780850	AZ828692	AZ432080
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% Query Match Length DB	25	26	28	29	30	24	27	23	23	27	28	28	21	25	56	28	29	59	27
% Query Match	55.8	55.8	54.2	53.3	51.7	50.8	50.8	50.0	50.0	50.0	50.0	49.2	48.3	48.3	48.3	48.3	48.3	48.3	47.5
Score	13.4	13.4	13	12.8	12.4	12.2	12.2	12	12	12	12	11.8	11.6	11.6	11.6	11.6	11.6	11.6	11.4
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AIII8404 AZ342196 TAZ05E06P AZ345594 CZ472219 CZ472219 CZ47221 AQ189071 AQ189071 AQ189071 AQ198505 AZ816143 AZ916143 AZ916143 AZ91615 CZ175615 CZ175615 CZ175615 CZ175615 CZ175615 AZ9198505 AZ942905 CZ1761134 AU014106 AU014106 AZ942905 CT014183 AZ942905	LIG 25 25 25 25 25 25 25 25 25 25 25 25 25
47.5 47.5 47.5 47.5 47.5 47.5 47.5 47.5 46.7 47.5 48.7	MOUSE 1 MOOOSNO GI:129 GI:129 GI:129 I; Muro
4.4.4.4.4.2.2.2.2.2.2.2.2.11111111118888	
	RESULT 1 AZ775852/c LOCUS DEFINITION ACCESSION VERSION KEYMORDS SOURCE ORGANISM TITLE JOURNAL COMMENT COMMENT BOUIC

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Gaps ö

EST 18-DEC-1999

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/clone lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar bet, library provided by KWS
Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
orientation:
Sep-Sal1-CCAGGGGTCGG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local Pi: Dr. Katharina Schneider, coordinator:
project, local Pi: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"
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(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pyTT3 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckgraefe (Washington University, dieck@im.wustl.edu); colonic mucosa represents a range of disease involvement from moderate to severe Crohn's disease; samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Fatima Bonaldo.
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we76d05.x1 Soares Dieckgraefe colon NHCD Homo sapiens cDNA clone
IMAGE:2347017 3' Fimilar to TR:O60318 060318 MCM3 IMPORT FACTOR ;,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (Dass 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Conne is available royalty-free through LLNL; contact the
IMAGE Consortium (infe@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 850 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 47.8<sup>th</sup>
Matches 11; Conservative
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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KEYWORDS
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AI673609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwb42 (gql #732114|gpl AF125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ586604 1inear EST 06-DEC-2002 E012388-024-012-E21-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-012-E21 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Beparatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

(bases 1 to 26)

Hervig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
         /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Wector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 26 Std Brror: 0.00
Plate: 12 row: B column: 21
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
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/db_xref="taxon:161934"
/clone="024-012-E21"
/tlshue_type="leaf"
/lab_host="EMDH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AUUGUCUCCUTUCGCCACCUC 24
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Matches 10; Conserv
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Query Match

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ORIGIN

RESULT 4 CL983097/c

DEFINITION

ACCESSION

VERSION KEYWORDS

SOURCE

REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gil #732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 S85 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 bp mRNA linear EST 01-AUG-2003
D08Bll_D23_04.abl cDNA Peking library 2, 4 day SCN3 Glycine max
CA850924
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                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Whouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wetcor: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddundegenetics.utah.edu
Insert Length: 10000 Std Brror: (
Plate: 0423 row: O column: 13
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UGCIM0423013"
                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 30.
Location/Qualifiers
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                      Mus musculus (house mouse)
Mus musculus
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Matches 9; Conserval
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                      SOURCE
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KEYWORDS
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Emax: +39081579030815790308
Email: cobellis@stigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
equence tag generated by 5' RACE of total RNA from gene trap ES
equence tag generated by 5' RACE of total RNA from gene trap ES
gene are available upon request from TIGEM. Annotation information
available from IIGEM
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1 (bases 1 to 29.

Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
                                                                                                    Gaps
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                                            Length 28;
                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Embryonic stem cell"
|cell_line="El4"
|/colo. | lib="TibBM gene trap library"
|note="Vector: pPLIP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Via P. Castellino, 111, 80131 NAPOLI, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177
                                               DB 1;
                                            54.2%; Score 13; DB 1;
38.1%; Pred. No. 5e+05;
iive 8; Mismatches
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clone="10662.60"
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/strain="129 ola"
                                                                                                                                                       1 UAUUGUCUCUCCUUUCGCCAC 21
                                                                                                                                                                                      B TCTGTTCTTCTTCTCCAC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
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AZ604126.1 GI:11726316
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                                                                      Best Local Similarity 38.1
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     nRNA sequence.
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Query Match

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LOCUS

ACCESSION

VERSION

AZ604126/c

RESULT 5

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/lab host-wate.
/lab host-wate.
/lab host-wate.
/clone_lib="Moouse 10kb plasmid UUGCIM library"
/clone_lib="Woouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerses and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose get a 9.5 to
10.5 kb range using preparative agarose get of plasmid All the vector was ligated
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Contact: RObert B. Weiss
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Tel: 801 S85 5606
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1M0054A13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0054A13 R, genomic survey sequence.
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Mus musculus

Mus musculus

Mus musculus

Muscapus, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,

Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
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                           0.00
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Brror: 0.
Plate: 0072 row: C column: 20
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid enda
High quality sequence stop: 27.
High quality sequence
                                                                                                                                                                                     1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0072C20"
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Alkharouf,N., Khan,R. and Matthews,B.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                       Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="DOBB11"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBlueecript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."
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1 (bases 1 to 27)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Tingey,A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
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Mus musculus
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     CA850924.1 GI:33387717
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                                                          Glycine max (soybean)
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Fax: 801 585 7177
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Fax: 301
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Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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11 TATTGTCTCTC 22
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                     /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: Purified genomic DNA from M. musculus G578L FWG (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 1.4e+06;
6; Mismatches 0; Indels
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: A column: 13
Seq primer: CACACAGGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 23.
                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC1M0054A13"
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                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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AZ514958
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8 g

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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adappored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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GC0348 TIGEM gene trap library Mus musculus cDNA clone 10863.13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 27)
Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Barbarisi, M., Sardiello, M., Di Giorgio, F. P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone llb="Mouse lokb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177
Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunmogenetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0054 row: A column: 13
                                                                                                                                                                           Seg primer: CGTTGTAAAACGACGGCAGT
Class: plaamid ends
High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                             /mol type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0054A13"
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Gape

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DME545811 28 bp DNA linear GSS 24-FEB-2003 Drosophila melanogaster flanking sequence of RS P element insertion P{RS3}CB-6297-3, clone library P{RS3}, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-FEB-2003) Ryder E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM The insertion point of the Pelement is before base 1 of the caquence. Further information about this P element insertion line can be found at http://www.flyseq.org.uk and http://www.drosdel.org.uk.
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mapping of RS P element insertions in Drosophila melanogaster for the Drosbal second generation deficiency kit Unpublished (pages 1 to 28)

    .28
/note="P element insertion in the 5' to 3' orientation"

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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryder, E.J., Ashburner, M., Bagunya, J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P., Mechler, B., O'Kane, C., Fflugfelder, G., Rasmuson-Lestander, A., Reurer, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and Russell, S.
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                                                                                            Length 28;
                                                                           49.2%; Score 11.8; DB 14; Length 60.0%; Pred. No. 1.7e+06; Live 4; Mismatches 2; Indels
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
                                                                                50.0%; Sco...
40.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS; genome survey sequence.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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/clone_lib="P{RS3}"
/note="read=5' end"
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                                                                                                                                                                                           1 UAUUGUCUCUCCUUUCGCCA 20
                                                                                                                                                                                                                       chromosome="3L"
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AJ545811.1 GI:28553693
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                                                                                                                                                 Conservative
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Matches 9; Conserv
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplanae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplanda;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
E. (bases II to 28)
E. (bases II to 28)
S. Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Longublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH901484 SALK 079650.53.10.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_079650.53.10.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Fax: +390815790919
Email: cobelisedrigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="SALK 079650.53.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                                                /cell_type="Embryonic stem cell"
|cell_line="El4"
|celone_lib="TIGEM gene trap library"
|note="Vector: pFLIP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis thaliana"
                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="10863.13"
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                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: TDNA tagged
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Gaps

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Email: Capbb-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clome_lib="NCI_CGAP_Ut3"
hote="Organ: uErus, Vector: pCMV-SPORT6; Site_l: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ454352 108S 04-OCT-200 DNA linear GSS 04-OCT-200 JM0256G18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0256G18 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                           Hominidae, Homo.

1 (bases 1 to 25)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, K., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2204055"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11.6; DB 1; Length 25;
Pred. No. 2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality Insert Length: 1192 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lab host="DH10B"
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AZ454352,1 GI:10612477
GSS.
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                                          GI:4453375
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                                                                                            Homo sapiens (human)
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Unpublished (1997)
                                                                                                                        Homo sapiens
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                                       AI539240.1
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                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rois, M., Rose, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIS39240 25 bp mRNA linear EST 13-MAY-1999 tp64b08.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2204055 3' similar to TR:Q40726 Q40726 DNA BINDING PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/clone_lib="Mouse 10kb plasmid UTGCIM library."
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0294 row: J column: 14
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0294J14"
                                                                Mus musculus (house mouse)
AZ475883.1 GI:10634008
GSS.
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Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
                                                                                                                                                                                                      (bases 1 to 21)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                            Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAD42 (gil 4732114|gb|AR12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xilio-Gold (Stratagene) cells and selected for ampicillin resistance."
                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Bex="Male"
/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse"
/clone_lib="Wotcr: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7176
Fax: 801 585
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/clone="UUGC1M0256G18"
Unpublished (2000)
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JOURNAL
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Gaps ö Query Match 48.3%; Score 11.6; DB 11; Length 26; Best Local Similarity 50.0%; Pred. No. 2.1e+06; Matches 9; Conservative 5; Mismatches 4; Indels (

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7 CUCUCCUTUCGCCACCUC 24

6 crcrccrcrcrcrcrc 23 g Search completed: October 16, 2006, 15:51:29 Job time : 1035.18 secs

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11; Conservative
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Best Local Similarity
Matches 11; Conserv
STRANDEDNESS:
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RESULT 1
 81941, A
10, Appl
10, Appl
10, Appl
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                                                                                                                                                                                                                                                                                                        Issued Patents NA:*

1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

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US-09-118-408-10
US-09-506-855-10
US-09-911-176B-10
US-09-619-740-10
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US-08-014-943A-15
US-08-486-421-20
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US-08-25-66-38
US-08-484-138-38
US-08-484-138-38
US-08-486-421-34
US-08-486-421-34
US-08-486-421-34
US-08-486-411-34
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        1403666 segs, 935554401 residues
           GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                  nucleic search, using sw model
                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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24
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Match
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Perfect score:
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APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: Cloning And Expression Of PUR Protein
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STRRET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10.036-2711
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.DOS
SOFTWARE: PARENIT RELOGATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.0%; Score 15.6; DB 2; Length 24; 50.0%; Pred. No. 6.4e+02; ive 7; Mismatches 4; Indels
US-09-198-452A-3360

US-09-506-852-10

US-09-396-196G-64399

US-09-396-196G-64399

US-09-396-196G-119671

US-08-45-426B-100

US-08-445-463B-56

US-08-445-463B-56

US-08-445-464C-57

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US-09-396-196G-14417

US-09-396-196G-14428

US-09-396-196G-11749

US-09-396-196G-11749

US-09-396-196G-11749
                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: 6923-033
RELECOMOUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-884/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/014,943A FILING DATE: 02) FEB) 1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-014-943A-3/c
; Sequence 3, Application US/08014943A
Patent No. 5545551
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,7
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GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US.A.
CIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-JUN-1995
ATFORNEY/AGENT INPORMATION:
NAME: CCPULZZ, LBULER 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-UN-1995
ATTORIEY/AGENT: NFORMATION:
ANALY AGENT: 1 NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 UNGUCUCUCCUTUCGCCACCUC 24
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; Sequence 38, Application US/08486421
; Patent No. 5672479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-
TELECOMUNICATION: INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 869-9741/88
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20: SEGUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 869-:
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                      US-08-014-943A-15
Sequence 15, Application US/08014943A
Sequence 15, Application US/08014943A
Patent No. 554551
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TILLE OF INVENTION: Cloning And Expression Of PUR Protein
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08486421
Patent No. 5672479
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                             COMPERSONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREE: 1155 Avenue of the Americas
CITY: New York
CUNTRY: 0.5.A.
ZIP: 10036-2711
ZIP: 10036-2711
ZIP: 10036-2711
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYBE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,943A
FILING DATE: 02) FEB11992
CLASSIFICATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-033
TELECOMMUNICATION NUMBER: 6923-033
TELEPHONE: 212 869-8864/9741
TELEPHONE: 212 869-8864/8741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 UNGUCUCUCCUUUCGCCACCUC 24
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                                                23 TTTTCTCCCTCCACCACCTC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
U.S.A.
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-486-421-20/c
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GENERAL INFORMATION:
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                                                                                                                                                                                  Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08470911
Patent No. 5756684
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 24;
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                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.0%; Score 15.6; DB 2; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4;
                                                                                                                                                                                Query Match 65.0%; Score 15.6; DB 2; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERNICE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                       2 TTTTCTCTCCCTCCACCTC 23
                                                                                                                                                                                                                                                                3 UNGUCUCUCCUUUCGCCACCUC 24
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Patent No. 5756684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS.
LENGTH: 24 base pairs
                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
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                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10036-2711
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US-08-470-911-20/c
                                                                                                                                          US-08-486-421-38
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APPLICANT: Begenann, Andrew D.
TITLE OF INDRINGS: Beared M.
APPLICANT: Begenann, Andrew D.
TITLE OF INDRIFTON: LOUNING AND EXPRESSION OF PUR PROTEIN
NUMBERS OF SEQUENCES: S.1
ADDRESSION SEQUENCES: S.1
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Gaps

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GENERAL INFORMATION:
APPLICANT: SUCOV, HENRY M
APPLICANT: EVANS, RONALD M
APPLICANT: EVANS, RONALD M
APPLICANT: UMESONO, KAZUHIKO
TITLE OF INVENTION: RESPONSE ELEMENT COMPOSITIONS AND ASSAYS EMPLOYING SAME
FILE REPERENCE: 08802/152,
CURRENT APPLICATION NUMBER: US/07/672,530C
CURRENT PILING DATE: 1991-03-19
RIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PARENT Ner: 2.1
SEQ ID NO : 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
Query Match 65.0%; Score 15.6; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 6.4e+02; Matches 11; Conservative 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 29;
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Patent No. 5558988

GRNERAL INFORMATION:

APPLICANT: Ala-Kokko, Leena

APPLICANT: Ala-Kokko, Leena

APPLICANT: Ala-Kokko, Leena

APPLICANT: Baldwin, Perti

APPLICANT: Baldwin, Clinton

APPLICANT: Hopkinson, lan

APPLICANT: Ahmad, Nilofer Nina

TITLE OF INVENTION: PREJISPOSITION FOR OSTEOARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide, M2
US-07-672-530C-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.7%; Score 14.8; DB 3;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 10; Conservative 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/977,284A FILING DATE: 13-NOV-1992
                                                                                                                                                                                                                                                           US-07-672-530C-16/c
; Sequence 16, Application US/07672530C
; Patent No. 6492137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                     2 TITICICICCICCACCIC 23
                                                                                                              3 unguedecucedunegeeactic 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 cucuccumceccaccuc
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-977-284A-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Johnson, Andrew D.
APPLICANT: Bergemann, Andrew D.
TILLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: TOUSTS-Z/II

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEN PC compatible
COMPUTER: TEN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,809
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/470,911
PILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CCTUZZI, LAULE A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 6923-053
TELEFPHONE: (212) 790-9090
TELEFPHONE: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
TELEX: G6141 PERNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUIBCIE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                                                 NAME: COTUZZI, LAUKA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 6141 PENNIE
STRANDENNESS: 81ngle
          APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/08486809
Patent No. 5869622
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
US-08-486-809-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 11; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: DNA
US-08-486-809-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-08-486-809-38
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Sequence 38, Application US/08484138 Patent No. 5622350 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 UAUUGUCUCUCCUUUCGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS: LENGTH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 TTTTATCTCTCCTTTCTCC
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Best Local Similarity 36.81
Best Local 7; Conservative
                        ; LENGTH: 18
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
US-08-256-426B-99
      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-484-138-38/c
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     60.0%; Score 14.4; DB 2; Length 18; 62.5%; Pred. No. 2.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 99, Application US/08256426B
Patent No. 5948611
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Milliams, Charlene J.
APPLICANT: Milliams, Charlene J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokno, Darwin J.
APPLICANT: Almad, Nolfer Nina
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM COMPALIALE
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORDERRECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,426B
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10964
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
FILING DATE: 13-NOV-1993
APPLICATION NUMBER: US 07/977,284
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: MATK DELUCA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark:
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-0697
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1082
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 CUCCUTUCGCCACCUC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CTCCTTTCCCCACCTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.0°
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                LENGTH: 18
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINEAR ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                           US-07-977-284A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-08-256-426B-99
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                                                1; Indels
                                                                                                                                                                                                                             US-08-242-664-38/c

Sequence 38, Application US/08242664

Patent No. 557139/

GENERAL INFORMATION:

APPLICANT: Watanabe, Kyoichi A.

APPLICANT: Weil, Weger

TITLE OF INVENTION: Complementary DNA and Toxins

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE:

CORRESPONDENCE ADDRESS:
Score 14.4; DB 2;
Pred. No. 2.1e+03;
Query Match 60.0%; Score 14.4; D
Best Local Similarity 62.5%; Pred. No. 2.1e
Matches 10; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
CLASSIFICATION: 514
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TILE OF INVENTION:
TILE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            Query Match 59.2%; Score 14.2; DB 7; Length 21; Best Local Similarity 36.8%; Pred. No. 2.7e+03; Matches 7; Conservative 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRING SISIENT Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,943A
FILING DATE: 0.2) FEB 1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 90,742
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
TELEFRAX: 212 869-8844/9741
TELEY: 641 PENNIE
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                            44683-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-014-943A-12/c
; Sequence 12, Application US/08014943A
; Patent No. 5545551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 UNGUCUCCUUNCGCCACCUC 24
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4468
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-391-0526
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                          1 UAUMGUCUCUCCUTUCGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 TTTATCTCTCCTTTCTCC 1
                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conservi
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TOPOLOGY: unk
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| Sequence 38, Application PC/TUS9506379
| GENERAL INFORMATION:
| APPLICANT: Watanabe, Kyoichi A.
| APPLICANT: Wati, Nu-Yun
| APPLICANT: Wati, Nu-Yun
| TITLE OF INVENTION: Complementary DNA and Toxins
| TITLE OF INVENTION: Complementary DNA and Toxins
| CORRESPONDENCES: 43
| CORRESPONDENCES: 135 Avenue of the Americas
  APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Mu-Yun
APPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PREENTIN STEEM: C-LOSY NG-LOS SOFTWARE: PREENTIN Release #1.24
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELECOMMUNICATION INFORMATION: TELEPAX: 212-64-0526
TELEFAX: 212-64-0525
INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06379
FILING DATE: May 13, 1994
                                                                                                                                                                                                             STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
1: New York
TRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-484-138-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: 1
STATE:
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Search completed: October 16, 2006, 14:47:14 Job time : 56.5789 secs

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"US-10-719-900-980988
; Sequence 980988, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AUUGUCUCCUUUCGCCACC 22
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Best Local Similarity 52.4,
Best Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-136-527-336045/c
FEATURE:
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1: KBMC Celerra_SIDS3/prodata/2/pubpna/US07_PUBCOMB.seq:*
2: KBMC Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq:*
3: KBMC Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq:*
4: KBMC Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq:*
5: KBMC Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq:*
6: KBMC Celerra_SIDS3/prodata/2/pubpna/US108_PUBCOMB.seq:*
7: KBMC Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCOMB.seq:*
8: KBMC Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCOMB.seq:*
9: KBMC Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCOMB.seq:*
10: KBMC Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCOMB.seq:*
11: KBMC Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCOMB.seq:*
12: KBMC Celerra_SIDS3/prodata/2/pubpna/US10B_PUBCOMB.seq:*
13: KBMC Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCOMB.seq:*
14: KBMC Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCOMB.seq:*
15: KBMC Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCOMB.seq:*
16: KBMC Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCOMB.seq:*
16: KBMC Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCOMB.seq:*
16: KBMC Celerra_SIDS3/prodata/2/pubpna/US11A_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 42579, A
Sequence 88871, A
Sequence 88877, A
Sequence 47774, A
Sequence 205339,
Sequence 276878,
Sequence 276878,
Sequence 276878,
Sequence 43878,
Sequence 21637, A
Sequence 21634, A
Sequence 21634, A
Sequence 21634, A
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                                                                                               October 16, 2006, 14:16:09; Search time 337.985 Seconds (without alignments) 872.534 Million cell updates/sec
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             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-719-900-980988

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US-10-956-157-88877

US-11-060-756-47784

US-11-136-527-276878

US-10-11-136-527-276878

US-10-11-36-527-276878

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US-10-130-914A-98782

US-10-956-157-21624

US-10-956-157-21634

US-10-956-157-21634
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Maximum Match 100%
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                                                                    OM nucleic - nucleic search, using sw model
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Match Length DB
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seq length: 30
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Perfect score:
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Sequence 2144, Ap Sequence 2144, Ap Sequence 2142, Ap Sequence 2142, Ap Sequence 2142, Ap Sequence 2143, Ap Sequence 2141, Ap Sequence 2141, Ap Sequence 2141, Ap Sequence 661177, Sequence 4236, A Sequence 4236, A Sequence 43354, A Sequence 43554, A Sequence 43554,
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Sequence 43359, A
Sequence 88872, A
Sequence 47765, A
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Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVERTION Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT FILING DATE: 2005-05-25

CURRENT FILING DATE: 2005-05-26

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

LENGTH: 25
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                                          OTHER INFORMATION: Probe US-11-136-527-336045
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ORGANISM: Artificial
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| Sequence 88877 | Application US/10956157 | Sequence 88877 | Application US/10956157 | Sequence 88877 | Application No. US20050118625A1 | Sequence 88877 | Application No. US20050118625A1 | Sequence 88877 | Application No. US20050118625A1 | Sequence 88877 | Sequence 888877 | Se
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| Sequence 4774, Application US/2050221354A1
| Sequence 4774, Application No. US20050221354A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| APPLICANT: Wyeth
| TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
| TITLE OF INVENTION: Target Genes
| TITLE OF INVENTION: UNBER: US/11/060,756
| CURRENT APPLICATION NUMBER: US/11/060,756
| CURRENT FILING DATE: 2005-02-18
| NUMBER OF SEC ID NOS: 303284
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Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
Target Genes
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45.8%; Pred. No. 4.5e+03;
tive 8; Mismatches 5;
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Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays
                                                                2 TATTGTCTCTCATAGCACCACATC 25
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                                1 UAUUGUCUCUCCUUUCGCCACCUC 24
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SEQ ID NO 47774
LENGTH: 25
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Best Local Similarity
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US-11-060-756-47774/c
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; ORGANISM: probe
US-11-060-756-47774
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VETSION 3.2
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REPRESNCE: 031986-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 980988
                                                                                                                                                                                                                                                                                                                                                                              Length 25;
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10; Mismatches 5;
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"Sequence 42579, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
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Best Local Similarity 37.5%
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Matches 11; Conservative
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Matches 11, Conservative
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US-10-956-157-42579
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US-10-956-157-88871
                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
US-10-719-900-980988
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US-10-956-157-88871
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Sequence 276903, Application US/11136527

PUBLICATION NO. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wounts, William M
TITLE OF INVENTION:
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

LENGTH: 25
                                    Gaps
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 678730
LENGTH: 25
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                                    Indels
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Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
ITILE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11.20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR APPLICATION NUMBER: 60/427,808
      47.4%; Pred. No. 5.5e+03;
tive 8; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.8%; Score 15.8; DB 16; Best Local Similarity 47.4%; Pred. No. 5.5e+03; Matches 9; Conservative 8; Mismatches 2;
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Best Local Similarity 45.5%; Pred. No. 6.7e+03;
Matches 10; Conservative 8; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 UNUNGUCUCUCCUUUCGCCACC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TATTGTCTCAGCTTTAGTCACC 23
                                                                                               2 AUUGUCUCUCCUUUCGCCA 20
                                                                                                                                       6 ATTGTCTGTCCTTTGGCCA 24
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                                 9; Conservative
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CRGANISM: Mus musculus
US-10-719-900-678730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                              RESULT 10
US-11-136-527-276903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                           임
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
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Sequence 276878, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AMA101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 276878
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Pred. No. 5.5e+03;
0; Mismatches 2; Indels (
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Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
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45.8%; Pred. No. 4...
... 8; Mismatches
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                             CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47788
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 205339, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:
      FILE REFERENCE: AM101083 (031896-042000)
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89.5%;
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Best Local Similarity 45.0.
Best Local 11; Conservative
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Best Local Similarity 89.59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Human
US-10-310-914A-205339
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                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-47788
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LENGTH: 24
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Query Match
Best Local Similarity
Matches 8; Conserv
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US-10-956-157-21624
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Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyech
APPLICANT: Wyech
APPLICANT: Would:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANTON
AUMBER: USTOO (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 21624
LENGTH: 25
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TITLE OF INVENTION: Baloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
LENGTH: 20
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                                       APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NOS: 991174
SEQ ID NOS: 991774
SEQ ID NOS: 991774
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US-10-310-914A-498782
; Sequence 498782, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AUVGUCUCUCCUUUCGCCACCU 23
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Best Local Similarity 94.1
Marches 16; Conservative
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Matches 9; Conservative
                       Alan
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ORGANISM: Probe Sequence
                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Mus musculus
US-11-036-317-35846
                       APPLICANT: Williams,
  GENERAL INFORMATION:
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US-10-310-914A-498782
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Sequence 21630, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES
FILE REPERENCE: 031896-043000 (AM 101081)
CURRENT PELLING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 21630
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    Length 25;
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64.2%; Score 15.4; DB 10;
47.1%; Pred. No. 8.2e+03;
iive 8; Mismatches 1;
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                                                 8; Conservative
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Matches 8; Conservative
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; ORGANISM: Probe Sequence
US-10-956-157-21630
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Sequence 35946, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAWURA, YOKIKO
APPLICANT: KODAWA, YUKIKO
APPLICANT: KODAWA, TOWKKO
APPLICANT: RUJIWURA, TOWKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 42.9
Matches 9; Conservative
RESULT 1
US-11-217-529-33285
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US-11-217-529-35946
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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861058,
                                                                           October 16, 2006, 14:16:55; Search time 53.2331 Seconds (without alignments) 842.395 Million cell updates/sec
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         GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-217-529-33946
US-11-348-413-247873
US-11-348-413-247873
US-11-348-413-247874
US-11-348-413-247874
US-11-348-413-247876
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US-11-348-413-485167
US-11-348-413-485168
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US-11-348-413-1129277
US-11-348-413-1129777
US-11-348-413-40425
US-11-348-413-40426
US-11-348-413-40426
US-11-348-413-40426
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Maximum Match 100%
Listing first 45 summaries
                                                       nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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                                                                                                                                                                                                                                                       seq length: 0
seq length: 30
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Perfect score:
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Maximum DB
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865459,
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              74489, 7
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: NAKAMURA, YOKIKO
APPLICANT: ASHIKARI, TOSHHHIKO
APPLICANT: ASHIKARI, TOSHHHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 33285
LENGTH: 25
                                                  978933
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                             US-11-348-413-618728
US-11-348-413-978933
US-11-348-413-95262
US-11-348-413-251673
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US-11-217-529-22641
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US-11-348-413-75095
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US-11-348-413-80887
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Publication No. US20060099612A1
GENERAL INFORMATION:
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APPLICANT: MOUNTS, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: US/11/349,445
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 247873
LENGTH: 25
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NAME/KEY: misc feature
LOCATION: (1)...(25)
OTHER INFORMATION: SEQ ID NO: 7205; WANDIUM2G; Start 113; Stop 137;
OTHER INFORMATION: 000000001100000
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NAME/KEY: misc_feature

LOCATION: LI)..[25]

OTHER INFORMATION: SEQ ID NO: 7205; WANOLUM2G; Start 114; Stop 138;

OTHER INFORMATION: 000000001100000
US-11-348-413-247873
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59.2%; Score 14.2; DB 9;
Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3;
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 247872
LENGTH: 25
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; Sequence 247874, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
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25 ATAGICICITITAGCCA 7
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                                                                                                                           TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-348-413-247873/c
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APPLICANT: Mouth, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/USO5/035471
PRIOR APPLICATION NUMBER: US/11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
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; Publication No. US20060099612A1
; Genteral INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAWURA, NORHHISA
APPLICANT: NAKAWURA, YORHINO
APPLICANT: KODAMA, YUKNO
; APPLICANT: KODAMA, YUKNO
; APPLICANT: KODAMA, YUKNO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/21,529
; CURRENT APPLICATION NUMBER: US 10/932,182
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR PILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 171625
; MANDEL ASSOCIATION NUMBER: US 10/932,182
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42.1%; Pred. No. 3.1e+03;
tive 8; Mismatches 3;
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         FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
LENGTH: 25
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; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-35946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-171625
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Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.1
Matches 8; Conservative
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US-11-217-529-171625/c
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US-11-348-413-247872/C
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APPLICANT: Myoune, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR PILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR PLING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 485166
LENGTH: 25
                                                                                                                                                                                                                                                                                       APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
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; OTHER INFORMATION: SEQ ID NO: 7205; WANOIUM2G; Start 117; Stop 141;
; OTHER INFORMATION: 00000001100000
US-11-348-413-247876
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Pred. No. 3.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: ECT/USOS/035471
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
NUMBER: US 60/615,573
SRIOR APPLICATION NUMBER: US 60/615,573
INUMBER: US 60/615,573
SRIOR APPLICATION NUMBER: US 60/615,573
LENGTH: 25
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                                                                                                                                                                                Sequence 247876, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
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Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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OTHER INFORMATION: probe
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OTHER INFORMATION: probe
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                      APPLICANT: Murphy, Bilen
APPLICANT: Olmsted, Stephen
APPLICANT: Olmsted, Stephen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE COF INVENTION: 131896-084100 (AM 10.1724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/US05/035471
PRIOR APPLICATION NUMBER: DS 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 247874
LENGTH: 25
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Onnered, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION WUMBER: US/11/348,413
CURRENT FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: CT/USO5/035471
PRIOR PILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
NUMBER OF SEQ ID NOS: 1276209
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LOCATION: (1). (25)
OTHER INFORMATION: SEQ ID NO: 7205; WANOIUM2G; Start 115; Stop 139;
OTHER INFORMATION: 000000001100000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (1). (25)
; OTHER INFORMATION: SEQ ID NO: 7205; WANOIUM2G; Start 116; Stop 140;
; OTHER INFORMATION: 000000001100000
US-11-348-413-247875
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47.4%; Pred. No. 3.1e+03;
:ive 7; Mismatches 3;
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Publication No. US20060160121A1
GENERAL INPORMATION:
APPLICANT: Wyeth
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Mounts, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 47.4
Matches 9; Conservative
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Best Local Similarity 47.4
Matches 9; Conservative
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OTHER INFORMATION: probe
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial
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US-11-348-413-247875/c
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: DCT/USOS/035471
PRIOR FILING DATE: 2006-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
RIOR FILING DATE: 2004-10-05
BRIOR PLING DATE: 2004-10-05
LENGTH: 25
LENGTH: 25
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| LOCATION: (1): [25]
| THEN INFORMATION: SEQ ID NO: 14505; WANOIUQIX; Start 1590; Stop 1614;
| OTHER INFORMATION: 000000000010000
| US-11-348-413-485634
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Best Local Similarity 47.4%; Pred. No. 3.1e+03;
Matches 9; Conservative 7; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.2%; Score 14.2; DB 9; Best Local Similarity 47.4%; Pred. No. 3.1e+03; Matches 9; Conservative 7; Mismatches 3;
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 485168
TYPE: DNA
TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 485634, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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OTHER INFORMATION: probe
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US-11-348-413-485635/c
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APPLICANT: Mounts, William M

APPLICANT: Murphy, Ellen

TITLE OF INVENTION: ROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES

FILE REFERENCE: 031896-084100 (AM 101724)

CURRENT APPLICATION WUMBER: US/11/348,413

CURRENT FILING DATE: 2006-02-07

PRIOR APPLICATION NUMBER: US 11/243,445

PRIOR PILING DATE: 2005-10-05

PRIOR FILING DATE: 2005-10-05

PRIOR FILING DATE: 2004-10-05

PRIOR FILING DATE: 2004-10-05

NUMBER OF SEQ ID NOS: 1276209

SEQ ID NO 485167

LENGTH: 25
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APPLICANT: Mounte, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR APPLICATION NUMBER: PCT/USOS/035471
PRIOR APPLICATION DATE: 2005-10-05
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                                                   | LOCATION: (1). (25)
| OTHER INFORMATION: SEQ ID NO: 14491; WAN01UQID; Start 1352; Stop 1376;
| OTHER INFORMATION: 00000000001000
| US-11-348-413-485166
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                                                                                                                                                              Score 14.2; DB 9; Length 25;
Pred. No. 3.1e+03;
7; Mismatches 3; Indels
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Pred. No. 3.1e+03;
7; Mismatches 3;
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                                                                                                                                                                Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
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Best Local Similarity 47.4%;
Matches 9; Conservative '
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                              NAME/KEY: misc_feature
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ORGANISM: Artificial
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US-11-348-413-485168/c
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Onnered, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2005-00-07
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
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LOCATION: (1): (25)
OTHER INDEMATION: SEQ ID NO: 7205; WANOIUM2G_at; Start 114; Stop 138;
OTHER INFORMATION: 000000001100000
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    Indels
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9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                             Sequence 861056, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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                                                                                 1 UAUUGUCUCUCCUUUCGCC 19
                                                                                                                           21 TATTGTCTTTTCTTCACC 3
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7; Conservative
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                                                                                                                                                                                                                                                                                     RESULT 15
US-11-348-413-861056/c
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Matches
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### APPLICANT: Murphy, Ellen

### APPLICANT: Olmsted, Stephen

### TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES

### TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES

### TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES

### TITLE OF INVENTION NUMBER: US/11/348,413

### CURRENT FILING DATE: 2006-10-05

### PRIOR PILING DATE: 2005-10-05

### PRIOR PILING DATE: 2004-10-05

### PRIOR PILING DATE:
                                                           APPLICANT: Wyell
APPLICANT: Wyell
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PRESENCE
TITLE OF INVENTION: PRESENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: 2006-02-07
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
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| LOCATION: (1)..(25)
| OTHER INFORMATION: SEQ ID NO: 2332; WANOIUMKM_at; Start 686; Stop 710;
| OTHER INFORMATION: 1111111100000000
| US-11-348-413-689385
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Pred. No. 3.1e+03;
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Pred. No. 3.1e+03;
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Best Local Similarity 47.4%;
Matches 9; Conservative
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Best Local Similarity
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E08992 132528 132528 AR181963 AR494659 AR4876 AR24876 AR79363 AR79363

AR032175 AR032177 BD007603

AR309121 AR372695 AR015990 AR082031 AR061363 AR108262

AX215299 Sequence
AX215300 Sequence
AR060081 Sequence
E08992 PCR primer.
132528 Sequence 48
143473 Sequence 48
143473 Sequence
AR44659 Sequence
AR44659 Sequence
AR44659 Sequence
AR4965 Sequence
AR93177 Sequence
BD007603 NematodaAR301217 Sequence
BD007603 NematodaAR301217 Sequence
AR03177 Sequence
AR03177 Sequence
AR03177 Sequence
AR0610151 Sequence
AR061053 Sequence
AR061053 Sequence
AR061053 Sequence

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BD232707 30 bp DNA linear PAT 17-JUL-2003 Therapeutic and diagnostic domain 1-beta-2GPI polypeptide and method of using the same.

BD232707 GI:33042477
                                                                                                                                                                                                                                                                                                                                                                               Majumder, K., Spytek, K.A., Tchernev, V.T., Colman, S.D., Padigaru, M., Zerhusen, B., Gusev, V., Burgess, C., Li, L., Malyankar, U.M., Gangolli, E., Stone, D., Macdougall, J., Smithson, G. and Ellerman, K. Novel proteins and nucleic acids encoding same Patent: WO 0194416-A 70 13-DEC-2001; Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .26
// Organism="synthetic construct"
// mol_type="unassigned DNA"
// Apse="toxon:32630"
// note="Ag1252 PCR Probe Sequence"
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                                                                                                                                                                                                                                                                                                                                               synthetic construct
synthetic construct
other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                 26 bp
Sequence 70 from Patent W00194416.
AX399122
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|:||| |:||| |:|||| | |:||::
22 CTGCAGCTGAGAGTGTCTGGTT 1
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ses 14; Conserv
Query Match
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BD232707
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  셤
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AX443910 Sequence
AX443910 Sequence
AX70823 Sequence
AX034378 Sequence
AX004751 Sequence
AX004751 Sequence
AX137020 Sequence
BD10561 Genes sen
177021 Sequence
BD10561 Genes sen
177021 Sequence
181112 Sequence
CS226910 Sequence
CS226910 Sequence
CS226910 Sequence
CS226910 Sequence
CS226910 Sequence
CS226918 Sequence
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BD232707 Therapeut
                                                           ; Search time 2092.41 Seconds (without alignments) 2597.742 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                ggguuaucugcaacugagag.....uuuucuggaugcagaguccu
         . GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                          6366136 segs, 31973710525 residues
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            nucleic search, using sw model
                                                           October 16, 2006, 13:57:30
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BD232707
AX443910
AX447886
AX730823
AX730823
AR008237
AR008237
AR137020
BR137020
BR131026
BR131026
BR131026
BR13112
CS226910
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CS188766
AX215298
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Match Length
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Perfect score:
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PAT 27-MAY-2002

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116219 Sequence 45 AR263223 Sequence 166705 Sequence 45

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Computer Generated Probe Sequence."
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Organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe
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18.6%; Score 15.8; DB 2;
Best Local Similarity 73.7%; Pred. No. 1.8e+06;
Matches 14; Conservative 3; Mismatches 2;
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Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
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Patent: WO 0215649-A 365 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
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Sequence 4341 from Patent W00216649.
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Sequence 365 from Patent WO0216649.
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DEFINITION Sequence 28 from patent US 6965010.
  23
                         25 UGGUUAAGGCGUCCCCAAGUUGGAAGGGC
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AX443910
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AR770823
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             Synthetic construct

Ches sequences; artificial sequences.

El (bases 1 to 30)

Lainnik, M.D.

Therapeutic and diagnostic domain 1-beta-2GPI polypeptide and method of using the same

AL Therapeutic and diagnostic domain 1-beta-2GPI polypeptide and method of using the same

AL JOLLA PHARMACEUTICAL CO

OS Artificial Sequence

PN JP 2002517245-A/8

PN JP 200251724-A/8

PN JP 20025174-A/7

PN JP 200251724-A/8

PN JP 20025174-A/7
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1 (bases 1 to 30)
Marquis,D.M., Iverson,G.M., Victoria,E.J., Jones,D.S. and
Linnik,M.D.
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Location/Qualifiers
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    .30
    Corganiam="synthetic construct"
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/db_xref="taxon:32630"

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Sequence 18 from patent US 6858210.
AR639871
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synthetic construct
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AR639871
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1 (bases 1 to 30)
Skolnick, M.H., Goddgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Skolnick, M.H., Goddgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Skolnick, M.H., Goddgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
and Futreal, P. Andrew.

17q-linked breast and ovarian cancer susceptibility gene
Patent: US 6162897-A 81 19-DEC-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.

1. (bases 1 to 30)
Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Harshman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.
and Putreal, P.Andrew.
170-linked breast and ovarian cancer susceptibility gene
Patent: US 575341.A 81 19-MAY-1998;
Harshman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W. and Futreal, P.Andrew.
17Q-linked breast and ovarian cancer susceptibility gene Patent: US 5747282-A 81 05-MAY-1998;
Location/Qualifiers
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Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6;
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AR008237
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/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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                                                                                                     1 (bases 1 to 28)
Altalo, K. and Jelsch, M.M.
Materials and methods involving hybrid vascular endothelial growth factor DNAs and proteins
Patent: US 6965010-A 28 15-NOV-2005;
Licentia, Ltd. and Ludwig Institute for Cancer Research; Helsinki; FIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alitalo, K.M. and Jeltsch, M.M.
Materials and methods involving hybrid vascular endothelial growth
factor dasa and proteins and screening methods for modulators
Factor WO 0162942-A 28 30-AUG-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia OY (FI)
Location/Qualifiers
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Unclassified.
1 (bases 1 to 30)
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
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64.0%; Pred. No. 2.6e+06;
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/mol type="unassigned DNA"
/mb xref="taxon:32630"
/noTe="oligonucleotide"
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synthetic construct
other sequences, artificial sequences.
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Sequence 81 from patent US 5747282.
AR004751
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AX234378
AX234378.1 GI:15593379

    .28
    /organism="unknown"
    /mol_type="genomic DNA"

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AR770823.1 GI:83346139
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PAT 10-JUN-1998

RESULT 11 BD105661 LOCUS

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1 (bases 1 to 30)
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Harshman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
17q-linked breast and ovarian cancer susceptibility gene
Patent: US 5710001-A 81 20-JAN-1998;
Location/Qualifiers
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Shattuck Eidens, D.M., Simard, J., Durocher, F., Emi, M. and Nakamura, Y.
Linked breast and ovarian cancer susceptibility gene Patent: US 5709999-A 81 20-JAN-1998;
Location/Qualifiers
                                                                          1 (bases 1 to 30)
Shattuck-Eidens, D.M., Simard, J., Durocher, F., Emi, M. and
                                                                                                                        Nationary Y.
Linked breast and ovarian cancer susceptibility gene
Patent: US $693473-A 81 02-DEC-1997;
Location/Qualifiers
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Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6;
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ilarity 36.0%; Pred. No. 2.6e+06;
Conservative 10; Mismatches 6;
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Sequence 81 from patent US 5710001.
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Sequence 81 from patent US 5709999.
181016
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/mol_type="unassigned DNA"
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Genes sensitive to 17g-chained breast cancer and ovarian cancer.
BD105661
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C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,C12N15/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 30)
Skolnick, M. H., Goldgar, D. E., Miki, Y., Swenson, J., Kamb, A., Harshman, K. D., Eidens, D. M. S., Tavtigian, S. V., Wiseman, R. W. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes sensitive to 17q-chained breast cancer and ovarian cancer Patent: JP 2001346591-A 79 18-DEC-2001, MYRIAD GENETICS INC, UNIVERSITY OF UTAH RESEARCH FOUNDATION, THE UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00,Cl2N5/00
Strandedness: Single;
Topology: Linear;
Genes sensitive to 17q-chained breast cancer and ovarian
                              Gaps
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Location/Qualifiers
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Best Local Similarity 36.0%; Pred. No. 2.6¢
Matches 9; Conservative 10; Mismatches
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Sequence 81 from patent US 5693473.
177021 GI:3013175
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JP 201346593-A/79
18-DEC-2001
18-APR-2001 JP 2001119644
12-AUG-1994 US 08/289221
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JP 2001346593-A/79.
Homo sapiens (human)
Homo sapiens
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AUTHORS
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PAT 10-JUN-1998

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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Methods, compositions and compound assays for inhibiting amyloid-beta protein production amyloid-beta protein production.
Patent: WO 2005103713-A 12 03-NOV-2005;
Galapagos Genomics N.V. (BE)
Location/Qualifiers
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                                 Query Match

18.1%; Score 15.4; DB 2; Length 30;
Best Local Similarity 36.0%; Pred. No. 2.6e+06;
Matches 9; Conservative 10; Mismatches 6; Indels
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Best Local Similarity 40.0%; Pred. No. 3.1e+06;
Matches 8; Conservative 9; Mismatches 3; Indels
                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                  CS226910 21 bp DNA Sequence 12 from Patent WO2005103713. CS226910.1 GI:83691771
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                              6 CTCTGCTTGTGTTCTCTGTCTCCAG 30
                                                                                                         55 CUUUGCUUCUGUUUUCUGGAUGCAG 79
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Homo sapiens
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CS226910
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Search completed: October 16, 2006, 14:52:14 Job time : 2094.41 secs

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Sequence 15707, A
Sequence 18, Appl
Sequence 2452, Ap
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81, Appl
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10621, A
20972, A
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                                                                                   October 16, 2006, 14:11:03; Search time 196.842 Seconds (without alignments) 807.979 Million cell updates/sec
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| FBMC Celerra SIDS3/ptodata/2/ina/1 COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/5 COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/6 COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/6 COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/7 COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/H COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/RE COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/RE COMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/ina/RE COMB.seq:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-328-199-18
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US-09-396-196G-119516
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US-09-396-196G-10620
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US-09-396-196G-20972
US-09-396-196G-20972
US-09-396-196G-20972
US-09-396-196G-20972
US-08-481-7818
US-08-55-10220-81
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Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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APPLICANT: Marquis, M. Gilbert
APPLICANT: Iverson, M. Gilbert
APPLICANT: Victoria, J. Edward
APPLICANT: Jones, S. David
APPLICANT: Linnik, Matthew
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC DOMAIN 1
TITLE OF INVENTION: (2GPI POLYPEPTIDES AND METHODS OF USING SAME FILE REFERENCE: 25231206900
CURRENT APPLICATION NUMBER: US/09/328,199
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US-09-396-196G-10302
US-09-396-196G-12190
US-09-396-196G-12191
US-09-396-196G-43541
US-09-396-196G-43541
US-08-396-196G-45033
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US-09-308-090-3
US-08-187-113-10
US-08-1886-161-10
US-08-1886-161-10
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Sequence 15707, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANT: David Mack
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 15707
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US-08-469-609A-45
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Patent No. 6858210
GENERAL INFORMATION:
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Best Local Similarity 60.0
Matches 15; Conservative
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ORGANISM: Mus musculus
US-09-396-196G-15707
 US-09-328-199-18
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US-09-306-19518
Sequence 119518, Application US/09396196G
Fatent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: AFFURCANT: NETDE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 119518
LENGTH: 25
LENGTH: 25
LENGTH: 25
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Pred. No. 1.1e+04;
8; Mismatches 5;
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Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mitmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affayerrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FABLESQ for Windows Version 4.0
SEQ ID NO 119517
LENGTH: 25
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45.8%;
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Best Local Similarity 50.0
Matches 11; Conservative
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; SEQ ID NO 119516
; LENGTH: 25
; TYPE: DNA
; CRGANISM: mus musculus
US-09-396-196G-119516
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US-09-396-196G-119517
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nes 11; Conserve
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19.1%; Score 16.2; DB 3; Length 30;
Best Local Similarity 58.6%; Pred. No. 9.7e+03;
Matches 17; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.8%; Score 16; DB 3; Length 25; 41.7%; Pred. No. 1.1e+04; cive 9; Mismatches 5; Indels
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Sequence 2452, Application US/09396196G
Sequence 2452, Application US/09396196G
Sequence 2452, Application US/09396196G
SEQUENCE NO SEQUENCE:
SECONDATE NO SEQUENCE:
SETTLE OF INVENTION: Methods of Genetic Analysis
SETTLE OF INVENTION: METHOD OF SEQUENCE:
SETTLE OF SEQUENCE: 1999-09-15
SETTLE OF SEQUENCE: 1998-09-17
SECONDATE: 1998-09-17
SEQUENCE: FRACE OF MINDOWS VERSION 4.0
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US-09-196G-119516

Sequence 119516, Application US/09196196G

Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
CHRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER: PSECTION NUMBER: 1998-09-17

NUMBER: PSECTION NUMBER: 1998-09-17

NUMBER: OF SECTION NOWER INDOMERTED
SOFTWARE: FRASEG for Windows Version 4.0
CURRENT FILING DATE: 1999-06-09

EARLIER APPLICATION NUMBER: 60/088,656

EARLIER FILING DATE: 1990-06-09

EARLIER FILING DATE: 1990-10-05

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PREESEQ for Windows Version 3.0

SEQ ID NO 18

LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGGTGATGGTGGCCACAACTTGGCATGGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 UGGUUAAGGCGUCCCCAAGUUGGAAGGGC 53
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic construct US-09-328-199-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 UUCUGUUUUCUGGAUGCAGAGUCC 84
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                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 41.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-2452
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LENGTH: 25
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Gaps

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Sequence 28, Application US/09795006A

Patent No. 6965010

GENERAL INFORMATION

APPLICANT Alitalo et al

TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS

FILE REFERENCE: 28967/35977B

CURRENT APPLICATION NUMBER: US/09/795,006A

PRIOR APPLICATION NUMBER: US 60/205,331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50927, Application US/09396196G
| Sequence 50927, Application US/09396196G
| Patent No. 682127, Application US/09396196G
| Patent No. 6821270.
| GENERAL INFORMATION:
| APPLICANT: Michael Mittmann
| APPLICANT: Mack
| APPLICANT: David Mack
| TITLE OF INVENTION: Methods of Genetic Analysis
| TITLE OF INVENTION: Methods of Genetic Analysis
| FILE REFERENCE: 3101.1
| CURRENT APPLICATION NUMBER: US/09/396,196G
| CURRENT FILING DATE: 1998-09-15
| PRIOR FILING DATE: 1998-09-17
| NUMBER OF SEQ ID NOS: 127806
| SEQ ID NO 50927
| LENGTH: 25
                                                         APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: David Lockhart
TILE CANT: Affymetrix, Inc.
TILE OF INVENITON: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 CAAGUUGGAAGGGCGCUUUGCUUCU 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAAGCTGGAAGGCCGCGAGGCTTAT 25
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25 CTTGTGTCATCTGTGAAGAGTCC 1
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: MUS musculus
US-09-396-196G-20972
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US-09-396-196G-50927/c
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Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
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                                                                                                                                                           Sequence 10620, Application US/09396196G; Patent No. 6821724; Patent No. 6821724; GENERAL INFORMATION: APPLICANT: Michael Mittmann; APPLICANT: David Mack; APPLICANT: David Lockhart; APPLICANT: David Lockhart; APPLICANT: Affymetrix, Inc.; TITLE OF INVENTION: Methods of Genetic Analysis; FILE REFERENCE: 310.1.1; CURRENT APPLICATION NUMBER: US/09/396,196G; CURRENT FILING DATE: 1999-09-15; PRIOR PELLING DATE: 1999-09-17; NUMBER OF SEQ ID NOS: 127806; SOFTWARE: FRAESEQ for Windows Version 4.0; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REPERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR PILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10621
LENGTH: 25
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68.0%; Pred. No. 1...
2; Mismatches
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Patent No. 682124
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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                                            63 CUGUUUUCUGGAUGCAGAGUCC
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Best Local Similarity 68.09
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Best Local Similarity 68.0°
Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-10620
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; ORGANISM: Mus musculus
US-09-396-196G-10621
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US-09-396-196G-10620
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US-09-396-196G-20972
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US-09-396-196G-10621
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APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Wiseman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 18.1%; Score 15.4; DB 2; Length 30; Best Local Similarity 36.0%; Pred. No. 2e+04; Matches 9; Conservative 10; Mismatches 6; Indels
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: 1201 New York Avenue, N.W., Suite 1000
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,553
FILING DATE:
                                                                                                               24884-109347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 CUUUGCUUCUGUUUUCUGGAUGCAG 79
ATTORNEY/AGENT INC......

NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2488.
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFRA: 202-962-8300
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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STATE: DC
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20005
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                                                                                                                                                                                                                                                                                                                        FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Artificial chimeric
OTHER INFORMATION: Oligonucleotide sequence derived from multiple vertebrate vascula
CTHER INFORMATION: endothelial growth factor
US-09-795-006A-28
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APPLICANT: Skolnick, Mark H.
APPLICANT: Skolnick, Mark H.
APPLICANT: Skolnick, Mark H.
APPLICANT: Skolnick, Mark H.
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Ramb, Alexander
APPLICANT: Alarthman, Keith D.
APPLICANT: Maeman, Roan V.
APPLICANT: Wiseman, Roan V.
APPLICANT: Fitzeal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
18.1%; Score 15.4; DB 4; Length 28;
Best Local Similarity 64.0%; Pred. No. 1.9e+04;
Matches 16; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
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CLASSITICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-MOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/185,205
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
SSOTWARE: Patentin Ver: 2.0
SEQ ID NO 28
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81, Application US/08480784 Patent No. 5693473
                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20002
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US-08-480-784-81
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APPLICANT: Miki, Yoshio
APPLICANT: Mamb, Alexander
APPLICANT: Ramb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Wiseman, Roger W.
APPLICANT: Putreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Succeptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Basetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.1%; Score 15.4; DB 2; Length 30; Best Local Similarity 36.0%; Pred. No. 2e+04; Matches 9; Conservative 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER EDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Pacentin Release #1.0, Version #1.30
SOFTWARE: Pacentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-UN-1995
CLASSIFICATION S14
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR.1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRICH DATA:
APPLICATION NUMBER: US 08/308,104
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
ATTINIG DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REPERENCE/DOCKET NUMBER: 24884-109347
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
TELEPHONE: 302-962-8300
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
SERANDEDENSS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS CUMUGCUMCUGUMUNCUGGAUGCAG 79
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Goldgar, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Emi, Mitsuru
APPLICANT: Emi, Mitsuru
APPLICANT: Durocher, Francine
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:.
APPLICATION NUMBER: US/08/487,002
  FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REFERENCE/DOCKET NUMBER: 24.89.57
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-962-4810
TELEFAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305

FILING DATE: 24-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824

FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104

FILING DATE: 16-SEP-1994

PRIOR APPLICATION NUMBER: US 08/300,266

FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CTCTGCTTGTGTTCTCTGTCTCCAG 30
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Patent No. 5710001
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Homo sapiens US-08-483-553-81
                                                                                                                                                                                                                                                                                                                               LENGTH: 30 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                     single
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COUNTRY: US
ZIP: 20005
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US-08-487-002-81
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Gaps

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FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/289,221
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffery L.;
REGISTRATION INFORMATION:
TELEPHONE: 202-962-8300
SEQUENCE THENACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORIGINAL SOURCE:
US-08-483-554B-81
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Search completed: October 16, 2006, 14:47:13 Job time : 197.842 secs

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                                                                                                               October 16, 2006, 14:04:23 ; Search time 3655.64 Seconds (without alignments) 1300.222 Million cell updates/sec
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                GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                              56556
                                                                                                                                                                                                                                                                                                          48236798 seqs, 27959665780 residues
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                        IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                  US-10-604-726A-6033
85
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gb_estl:;
gb_estl:;
gb_estle:;
gb_estle:;
gb_estle:;
gb_estle:;
gb_gssl:;
gb_gssl:;
gb_gssl:;
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                     Run on:
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		4			Solution	
		Query	:	;	ŧ	
ti i	Score	Match	Match Length DB	80	a a	Description
-	6.2	19.1	25	13	CZ910028	CZ910028 4018012H1
	16	18.8	30	10	H25855	H25855 y153h05.81
-i	15.4	18.1	22	11	AZ814281	AZ814281 2M0082L04
H	5.4	18.1	28	11	AZ583022	AZ583022 1M0376A16
Ă	4.6	17.2	25	σ	D19580	D19580 MUSGS00987
À	4.4	16.9	29	11	BZ292979	BZ292979 SALK 1290
À	4.2	16.7	20	11	AZ469472	AZ469472 1M0283A06
À	14.2	16.7	23	11	AZ785027	AZ785027 2M0028H03
	14	16.5	24	11	AZ806300	AZ806300 2M0068F13
H	3.4	15.8	56	7	BF732161	BF732161 EST-NGR-1
$\vec{\mathbf{H}}$	13.4	15.8	27	11	AZ763057	AZ763057 1M0558C22
H	3.4	15.8	27	14	AJ591134	AJ591134 Arabidops
H	3.4	15.8	29	11	BH792654	BH792654 SALK 0648
H	3.4	15.8	29	11	BH809983	BH809983 SALK 0368
н	3.2	15.5	27	σ	DN955347	DN955347 it86c09.g
H	3.2	15.5	28	н	AA961904	AA961904 or68c12.s
H	3.2	15.5	28	13	CZ482297	CZ482297 e04545-5p
H	3.2	15.5	28	14	ATH531105	AJ531105 Arabidops
-	3.2	15.5	29	13	CZ471342	CZ471342 d00034-5p

13 15.3 30 11 ATH527468 AZ788334 AZ78834 AZ788334 AZ788334 AZ788334 AZ78834 AZ788344 AZ78834 AZ78834 AZ78834 AZ78834 AZ788344 AZ788344 AZ788344 AZ788344 AZ788344 AZ788344 AZ788344 AZ788334 AZ788344 AZ788344 AZ788344 AZ788344 AZ7883434 AZ7883434	ALIGNMENTS /C CZ910028	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. I (bases 1 to 25) NRS Walbot, V. Maibot, V. Maibot, V. E maic genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V. Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Email: walbot Gestanford.edu Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 4018012 row: H column: 11 Class: transposon-tagged. Calitivar="mixed background W23/A188/B73/K55" Anol_type="genomic DNA" Anol_type="genomic DNA" Anol_type="genomic DNA" Anol_type="genomic DNA" Anol_type="genomic DNA" Anol_type="adult" Abo_nost="mixed background Grid X" Alb_host="mixed Grid X" Alb_host="mixed background Grid X" Alb_
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 COZ10028/c LOCUS DEFINITION ACCESION VERSION VERYWORDS SOURCE ORGANISM	ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES BOULT

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Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web units. For more information on RescueMu, go to the web site 'http://www.murtansposon.org/project/RescueMu/'. Grid X was grown at UCSD in 2003. DNA was extracted from leaf atrips, double digested using Bamali and Balli, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 bp mRNA linear EST 10-JUL-1995 yl53h05.81 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:162009 3' similar to gb:S71043_rna1 IG ALPHA-2 CHAIN C REGION (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Insert Size: 934
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMACE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 934 Std Error: 0.00
Seq primer: Promega -21m13
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.

1 (Dases 1 to 30)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                           19.1%; Score 16.2; DB 13; Length 25; 38.1%; Pred. No. 1.3e+06;
                                                                                                                                                                                                                                                           Indels
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ښ
                                                                                                                                                                                                                                                           10; Mismatches
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/mol_type="mRNA"
/db_xref="dDB:576220"
/db_xref="taxon:9606"
/clone="IMAGE:162009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 1.
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                                                                                                                                                                                                                                                                                                       50 GGGGGUUUGCUUCUGUUUUC 70
                                                                                                                                                                                                                                                                                                                                  23 GGCTCTTTGTTTTGTTTTC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ′вех="Реша]е′
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H25855.1 GI:894978
                                                                                                                                                                                                                                                           Conservative
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6
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
H25855/c
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Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]APL29072.1), a copy number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 22)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacree, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 20-FEB-2001
and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot 20. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ814281
2M0082L04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0082L04 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UGCIM library" /note="Vector: PWD42nv; Purlfied genomic DNA from M.musculus Cs7BL/63 (male) was obtained from the Jackson
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       ö
                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunngenetics.utah.edu
Constr. Length: 10000 Std Error: 0.00
Plate: 0082 row: L column: 04
                                                                                                                                                                   Query Match 18.8%; Score 16; DB Best Local Similarity 66.7%; Pred. No. 1.5e Matches 16; Conservative 3; Mismatches
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC2M0082L04"
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Location/Qualifiers
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AZ814281.1 GI:12984285
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AZ814281
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored to competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ583022 28 bp DNA linear GSS 13-DEC-2000 1M0376A16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0376A16 R, genomic survey sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                       Score 15.4; DB 11; Length 22; Pred. No. 2.3e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.0
Plate: 0376 row: A column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualiflers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0376A16"
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AZ583022.1 GI:11702488
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4 TTCTGTTTTCTGGAAGC 20
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                                                                                                                                                                                                                                                                                         61 UUCUGUUUUCUGGAUGC
                                                                                                                                                                                                                                           8; Conservative
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Fax: 801 585 7177
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Best Local Similarity
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KEYWORDS
SOURCE
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AZ583022
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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 3'-directed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sclurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                      25 bp mRNA linear EST 09-FEB-2
MUSGS00987 Mouse 3'-directed Mus musculus cDNA clone mb1686 3',
mRNA sequence.
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Contact: Shoko Kawamoto
Institute for Cellular and Molecular Biology
                                                                                                                                                                  ch 18.1%; Score 15.4; DB 11;
1 Similarity 44.0%; Pred. No. 2.4e+06;
11; Conservative 8; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: shoko@next.imcb.osaka-u.ac.jp.
Location/Qualifiers
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/clone="mb1686"
                                                                                                                                                                                                                                                       56 UUUGCUUCUGUUUUCUGGAUGCAGA 80
                                                                                                                                                                                                                                                                               2 TTCCTCCAGGTTTCTGAATGCAGA 26
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/strain="C57BL/6J"
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22 CTTTTCTTTTTTTGTGGAT 2
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BZ292979
BZ292979.1 GI:24340856
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KEYWORDS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMA2 (gil 4732114[gb]AR12972.1); a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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2M0028H03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M002BH03 R, genomic survey sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Roal, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Suright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                  /lab host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Plate: 0283 row: A column: 06
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
                                                                                                                                                                                /organism="Mus musculus
                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0283A06"
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Fax: 801 585 7177
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Best Local Similarity
Matches 6; Conserv
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/clone="SALK 129051.26.25.x"
/clone="SALK 129051.26.25.x"
/clone="lb="Axabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 29)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                          Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Railly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Mouse whole genome scaffolding with paired end reads from 10kb
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16.9%; Score 14.4; DB 11; Length 29;
Best Local Similarity 37.5%; Pred. No. 5.2e+06;
Matches 6; Conservative 9; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecoType="Col-0"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of puble [4732114 [gb] AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Joseph St. (2017). Clark, T., Lee, S., Zhou, G., Beer, C., Rowley, J.D. and Wang, S.M.
Rowley, J.D. and wang, S.M.
Pattern of gene expression in mouse GR-1+ myeloid progenitor cells Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse_lokb plasmid UGCIM library." /note="Wector: PWD4ZLY; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Fel: 773-702-6788
Fax: 773-702-3002
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   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: F column: 13
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/63"
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                                                                                                                                                                                               High quality sequence stop: 24.
Location/Qualifiers
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/clone="UUGC2M0068F13"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia; Eutheria; Euarchontoglizes; Glizes; Rodentia;
Sciurognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 24)
10 (bases 1 to 24)
11 (bases 1 to 24)
12 (bases 1 to 28)
13 (bases 1 to 28)
14 (bases 1 to 28)
15 (bases 1 to 28)
16 (bases 1 to 28)
17 (bases 1 to 28)
18 (bases 1 to 28)
18
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/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42tv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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           Std Error: 0.00
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Insert Length: 10000 Std Error: C
Plate: 0028 row: H column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                  xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UUGC2M0028H03"
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Similarity 63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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Tel: 801 585 5606
Fax: 801 585 7177
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genomic survey sequence.
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Balzergue, S.
Direct Submission
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AJ591134/c
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1M0558C22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic cone UUGCIM0558C22 F, genomic survey sequence.
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fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till the last CATG site of the target cDNA sequence. Seq primer: M13 Porwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus muscullus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UNGIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 27)
Dunn,D., Acyagi,A., Barber,M., Beaccrn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                       /tissue_type="bone marrow"
/cell_type="GR-1+ myeloid progenitor cells"
/clone_lib="mouse GR-1+ myeloid progenitor cells cDNA
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
linsert Length: 10000 Std Error: 0.00
Plate: 0558 row: C column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
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/mol_type="qenomir nwx"
                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
High quality sequence stop: 27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UUGC1M0558C22"
/bex="Male"
                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                      Library
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwhoz (gql 4742114[gb]AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. ool Xillo-Gold (gratagene) cells and selected for ampicillin resistance."
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FOR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoingen.fr).
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Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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SSS. 1eft border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Busaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/cctype="Wassilewskija"
1. .27
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="580B05"
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EMBO Rep. 3 (12), 1152-1157 (2002)
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LOCUS

RESULT 13 BH792654/c

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SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

ACCESSION VERSION

KEYWORDS

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DN955347 27 bp mRNA linear EST 04-MAY-2005
it86c09.gl Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetophyta; Gnetales; Gnetaceae; Gnetum.
1 (base 1 to 27)
Brenner, B.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. [1 (bases 1 to 29)]
                                                                                                                                                                                                                                                                        Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
A. Simmerman, J. and Ecker, J.R.
A. Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/clone="SALK 036896"
/clone="SALK 036896"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used car
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of
thaliana genomic clone SALK_036896, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 13.4; DB 11; Length 29; ilarity 43.5%; Pred. No. 1.1e+07; Conservative 7; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Arabidopsis thaliana"
                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: TDNA tagged.
Location/Qualifiers
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BH809983.1 GI:20387800
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/clone="SALK 06449.48.70.x"
/clone="lb="Txabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Bukaryotsi, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II, Brassicales; Brassicaeae; Arabidopsis.

| (bases 1 to 29)
Alonso, Ju., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
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                                                                                                           Length 27;
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
The Salk Studies Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                        Score 13.4; DB 14;
Pred. No. 1.1e+07;
3; Mismatches 1;
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/note="T-DNA flanking sequence
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/ecotype="Col-0"
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                       left border'
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                                                                                                        Query Match
Best Local Similarity 73.3
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Aei82438 Human mic Aas12826 Human VEG

Adx84134 DNA ampli Adk75812 Chimeric Adg(7714 Anti-NRID Aee01688 G procein Aee01688 G procein Act/4315 Human mic Aee67632 Human Hun Adx99810 PCR prime Abk00741 Human NOG Abk00742 Human NOG Abk00742 Human NOG Abk00742 Human NOG Abk0746 Sequence Abay8930 Dengue vi Act/8730 Dengue vi Act/8730 Dengue vi Act/8730 Human IRT Act/8730 Bengue vi Act/88550 Human mic Abb89358 Human mic

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	Description	Aad25159 Human NOV	Adk51090 Human NOV	Ade03643 BGS PCR p	Aah74161 Human neu	Aaz29694 Oligonucl	Aed56453 Human ost	Abq11002 Oligonucl	Abq04674 Oligonucl	Abq04715 Oligonucl	Abq00358 Oligonucl	Abg11043 Oligonucl	Abq12538 Oligonucl	Abg12579 Oligonucl	PCR	Ady03184 PCR prime	Adx84276 DNA ampli	Aed57194 Human ost	Aed57246 Human ost
SUMMARIES	ID	AAD25159	ADK51090	ADE03643	AAH74161	AAZ29694	AED56453	ABQ11002	ABQ04674	ABQ04715	ABQ00358	ABQ11043	ABQ12538	ABQ12579	ADY01452	ADY03184	ADX84276	AED57194	AED57246
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	Score	17.2	17.2	16.2	16.2	16.2	16.2	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.6	15.6	15.6	15.6	15.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated nucleic acids encoding polypeptides, designated NOVX polypeptides. The NOVX polypeptide and nucleic acid are useful for treating cardiomyopathy, atherosclerosis, diabetes or a disorder related to cell signal processing and metabolic pathway modulation. The NOVX polypeptide, nucleic acid and antibody are useful for treating or preventing a syndrome, e.g. various tissue/organ inflammation, muscular discases, cagulation disorders, cancers diseases, cardiovascular diseases, cagulation disorders, cancers (leukaemia, adenocarcinoma), multiple sclerosis, respiratory diseases, reproductive disorders, allergy, seizures, mental depression, epilepsy, gastro-intestinal diseases, bone disorders, nephrological disorders, urinary system disorders, immunological disorders, disease, urinary system disorders, and bronchitis. The present sequence is a probe
                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful for treating a syndrome associated with a NOVX-associated disorder, e.g. cardiomyopathy, atherosclerosis, neurological and neurodegenerative
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L, Malyankar UM, Gangolli E;
Ellerman K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOVX protein-related oligonucleotide probe SeqID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 BP; 8 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used for assessing human NOV4 gene expression
                                                                                                                                                                                                        Tchernev VT,
irgess C, Li
                                                                                                                                                                                                                             Burgess C, Li
Smithson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 151; 189pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CUGCAACUGAGAGGGGCUGGUU 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 CTGCAGCTGAGAGTGTCTGGTT 1
26-JUN-2000; 2000US-02141023P.
26-JUN-2000; 2000US-0214150P.
29-JUN-2000; 2000US-0215005P.
20-FEB-2001; 2001US-027060P.
26-FEB-2001; 2001US-0271623P.
26-MAR-2001; 2001US-0271631P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2002; 2002US-00115479.
05-APR-2002; 2002US-0370349P.
04-APR-2002; 2002US-0370569P.
12-APR-2002; 2002US-0372019P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-2003; 2003WO-US010142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK51090 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                     Majumder K, Spytek KA,
Zerhusen B, Gusev V, B
Stone D, Macdougall J,
                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                 WPI; 2002-062612/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003083046-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                  diseases
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AC ADK5108
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KW CYC
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Mes; primer; PCR; human; immunoglobulin; Ig superfamily; BGS;

We aberrant immunoglobulin cell surface receptor activity;

We dellular adhesion disorder; hyper-immunoglobulin receptor activity;

We productive disorder; female reproductive disorder; ovarian disorder;

We reproductive disorder; female reproductive disorder; ovarian disorder;

We reproductive disorder; female reproductive disorder; ovarian disorder;

We reproductive disorder; female reproductive disorder; ovarian disorder;

We pelvic inflammatory disease; endometriosis; premature menopause;

We pelvic inflammatory disease; endometriosis; premature menopause;

We aberrant androgen metabolism; polycystic ovarian disease;

Mesistant-ovary syndrome; hermaphroditism; immunodeficiency;

We resistant-ovary syndrome; hermaphroditism; immunodeficiency;

Mesistant-ovary syndrome; hermaphroditism; immunodeficiency;

Mesistant-ovary syndrome; hermaphroditism; disease;

Mesistant-ovary syndrome; hermaphroditism; desease;

Mesistant-ovary syndrome; arthritis; acthma; immunodeficiency;

Mesistant-ovary syndrome; hermaphroditism; dadised cytotoxicity;

Mesistant-ovary syndrome; autoimmune inflammatory bisease;

Mesistant-ovary syndrome; autoimmune inflammatory eye disease;

Mesistant-ovary syndrome; mesistant-ovary syndrome;

Mesistant-ovary syndrome;

Mesistant-ovary syndrome;

Mesistant-ovary syndrome;

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Mesistant-ovary syndro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to novel isolated polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic activity (as NoVX-agonists or antagonists) or vaccines. In addition, the disclosed sequences may be useful for gene therapy. The polypeptide is useful for preparing a composition for treating or preventing a pathological state in a mammal, for example cancer or for chromsome mapping. The present sequence is that of an oligonucleotide probe which was used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer or for chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                  P, Boldog FL, Burgess CE, Casman SJ, Furtak K;
thberg BE, Gunther E, Heyes MP, Li L, Spytek KA;
Malyankar UM, Edinger SR, Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 BP; 8 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example C; SEQ ID NO 111; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CUGCAACUGAGAGGGGCUGGUU 29
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                                                                                                                                                                                                                                                                                                                                                                                                        Anderson DW, Bento P, Boldog
Gorman L, Gould-Rothberg BE,
Stone DJ, Zhong M, Malyankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sjogren's disease; scleroderma.
                                     2002US-00160619.
2002US-0403748P.
2002US-00287226.
2003US-00403161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
2002US-0384543P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE03643 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-812539/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rothenberg ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention.
                                     03-JUN-2002;
15-AUG-2002;
04-NOV-2002;
31-MAR-2003;
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The invention relates to an isolated mucleic acid molecule encoding BGS-
2, 3 and 4 polypeptides. The nucleic acid molecule, polypeptide and methods are useful for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell sufface receptor activity; a cellular adhesion disorder; a disorder related to hyper- or hypo-immunoglobulin receptor activity; a disorder related to berrant signal transduction; a reproductive disorder; as ovarian disorder; ovarian cancer; sexual dysfunction; infertility; pelvic inflammatory disease; endometriosis; premature menopause; placental dysfunction; hormone deficiency; osetrogen deficiency; aberrant androgen metabolism; polycystic ovarian disease; aberrant ovarian cycle; dysfunctional uterine bleeding; resistant-ovary syndrome; hermaphroditism, immune disorders; inflammatory disorders; arthritis; asthma; immunodeficiency diseases uch as ADS; leuksemia; cinflammatory bowel disease; sepsis; acne; psoriasis; hypersensitivity; such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues; or autoimmunity disorders; autoimmune infertility; Addison's Disease; heamolytic anaemia; rheumatoid arthritis; dermatitis; graves; bases; haemolytic anaemia; insulin dependent diabetes mellitus gravis; insulin dependent diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid molecule encoding BGS-2, 3 and 4 polypeptides, useful for preventing, treating or ameliorating a medical condition, e.g. a disorder related to aberrant immunoglobulin cell surface receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune inflammatory eye disease; Sjogren's disease; and sleroderma. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.1%; Score 16.2; DB 10; Length 23; 38.1%; Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23 BP; 2 A; 4 C; 5 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.1%; Preα. ως.
-ive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 228; 242pp; English
                                                                                                                                                                                                                                                                                                      Feder JN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 GCGCUUUGCUUCUGUUUUCUG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||:::| :: :|::: |:|
GCGCTTTGATTATGTTTCCTG 21
                                                                                          .1-JUL-2002; 2002US-00193477
                                                                                                                            11-JUL-2001; 2001US-0304888P
12-APR-2002; 2002US-0372147P
                                                                                                                                                                                                                                                                                                      Lee L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH74161 standard; DNA; 29
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                                                                                                                                                                                       WUS.
KRYSTEKSR.
                                                                                                                                                                                                                                                                                                                                            WPI; 2003-844480/78
                                                                                                                                                                                                                                             FEDER J N.
CHENG J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                      Krystek SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
                   US2003195163-A1
                                                       16-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                           activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                     (WUSS/)
                                                                                                                                                                                                                                                               CHEN/)
                                                                                                                                                                                                                             LEEL/)
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ID AAH741
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DT 09-OCT
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The present invention provides the cDNA sequence of human neuronal calcium sensor protein 1 (NCS-1). The NCS-1 protein is a member of the neuronal calcium ion binding protein family and a homologue of human NCS-

Human neuron calcium sensing protein and its code sequence, preparation

Yu L, Fu Q, Zhao Y; WPI; 2001-398934/43.

(UYFU-) UNIV FUDAN.

99CN-00118819, 99CN-00118819.

07-SEP-1999; 07-SEP-1999;

14-MAR-2001

Unidentified

CN1287171-A.

Example 4; Page 13 (Disclosure); 21pp; Chinese

and use

Cheng JD;

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1. The present invention also relates to the protein, the application of the polynucleotide and the polypeptide, and the production process of the polynucleotide and the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide B2del242-326 for domain deletion mutant of hbeta-2 GPI.
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta-2 glycoprotein I; hbeta-2 GPI; beta-2 GPI domain 1; oligonucleotide B2de1242-326; sushi domain; beta-2 GPI-dependent antiphospholipid antibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linnik MD;
                                                                                                                                                                                                                                                                                                              19.1%; Score 16.2; DB 4; Length 29; 58.6%; Pred. No. 4.4e+04; ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Victoria EJ, Jones DS,
                                                                                                                                                                                                                                                                                           Sequence 29 BP; 6 A; 8 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                      14 CUGAGAGGGCUGGUUAAGGCGUCCCCAA 42
                                                                                                                                                                                                                                                                                                                                                                  29 CTACGACGGGCTGGTATAGGAATTCCCAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ29694 standard; DNA; 30 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0088656P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                         Local Similarity 58.6
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iverson GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-116542/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-1998;
08-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuronal calcium sensor protein 1 related oligonucleotide #6.
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Indels

Human; neuronal calcium sensor protein 1; NCS-1; primer; ds

Gaps

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Indels

88

RESULT 6 AED56453

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The invention relates to an oligonucleotide array (1) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABO00010-ABO13409. (1) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABO0010-ABO13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid above method is useful for detecting a target nucleic acid with (1). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                      Score 16.2; DB 14; Length 30; Pred. No. 4.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 6; Length
Pred. No. 5.9e+04;
3; Mismatches 2; Indels
               Seguence 30 BP; 4 A; 3 C; 12 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide array; adapter sequence; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide adapter/capture probe 10993
                                                                                                      9; Mismatches
                                                                                                                                                 69
                                                                                                                                                                          1 ACGITGGATGAGTGCTTTGCAGGTGTTGT 29
                                                                                                                                                 41 AAGUUGGAAGGCCCUUUGCUUCUGUUUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 225; 261pp; English.
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GAGAGGCGTTGGTTAAGGC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAGGGCUGGUUAAGGC 34
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                                                                                                                                                                                                                                                                                                    ВР
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2000US-0228854P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.6%;
                                                                               ilarity 41.4%;
Conservative
                                                             19.1%;
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                                                                                                                                                                                                                                                                                                    ABQ11002 standard; DNA; 24
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                                                                             Local Similarity
ses 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-AUG-2000;
29-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
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                                                                                                                                                                                                                                                                                                                                                  AB011002;
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                                                             Query Match
                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of identifying a subject at risk of osteoarthritis which comprises detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample where the presence of the polymorphism indicates a risk of osteoarthritis. The method is useful for identifying a subject at risk of osteoarthritis. The method is also useful for identifying a subject at for treating osteoarthritis. The present sequence represents a for treating osteoarthritis. The present sequence represents a PCR primer used to identify single nucleotide polymorphisms associated with
                                                                                                                          domain deletion mutant of human beta-2 glycoprotein I. Isolated domain I of beta-2 GPI binds to and inhibits beta-2 GPI-dependent antiphospholipid antibodies. Amino acids 242-326 are deletered from beta-2 GPI and the resulting protein contains 1, 2, 3 and 4 sushi domains. This is used to determine the antigenic regions of beta-2 GPI
                                                                                          sequence is oligonuclectide B2de1242-326 used for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a subject at risk of osteoarthritis comprises detecting the presence or absence of one or more specified polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Langdown ML;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteoarthritis; musculoskeletal disease; Antiarthritic; Osteopathic;
RNAi; RNAi interference; ADAMTS2 agonist; ss; PCR; primer.
New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting antiphospholipid antibodies for treating, e.g. thrombosis.
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                                                                                                                                                                                                                                                                                              Score 16.2; DB 3; Length 30;
Pred. No. 4.5e+04;
4; Mismatches 8; Indels
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                                                                                                                                                                                                                                                           Sequence 30 BP; 6 A; 6 C; 11 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human osteoporosis related SNP primer #413.
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                                                                                                                                                                                                                                                                                                                                                                                             25 UGGUUAAGGCGUCCCCAAGUUGGAAGGGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 88; 539pp; English.
                                                               Example 1; Page 51; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-2004; 2004US-0559011P.
01-APR-2004; 2004US-0559040P.
01-APR-2004; 2004US-0559902P.
01-APR-2004; 2004US-0559202P.
01-APR-2004; 2004US-0559203P.
01-APR-2004; 2004US-0559203P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.6%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2005100604-A2
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                                                                                                          The present
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Gaps

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2; Indels

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The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
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target nucleic acid sequence, has different addresses comprising
different specific capture probes.
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Pred. No. 5.9e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide adapter/capture probe 349.
                                                                                                                                                                     Claim 1; Page 147; 261pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 gagaggggcugguuaaggc 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GAGAGGCGTTGGTTAAGGC 3
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29-AUG-2000; 2000US-0228854P.
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Best Local Similarity 73.7%;
Matches 14; Conservative
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                (ILLU-) ILLUMINA INC.
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                                                                         WPI; 2002-292068/33
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                                              Gunderson K;
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                                                                         Oligonucleotide array; adapter sequence; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide adapter/capture probe 4706.
                                           Oligonucleotide adapter/capture probe 4665.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 147; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GAGAGGGCUGGUUAAGGC 34
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GAGAGGCGTTGGTTAAGGC 22
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2000US-0228854P.
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29-AUG-2000; 2000US-0228854P.
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              (first entry)
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                11-JUN-2002
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Gaps

ABQ12538 standard; DNA; 25

RESULT 12

ABQ12538;

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nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ1409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (1). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid.
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Pred. No. 5.9e+04;
3; Mismatches 2; Indels
                                                                                                                                         Score 15.8; DB 6; Length 24; Pred. No. 5.9e+04;
                                                                                                                                                                           2; Indels
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                                                                                                         Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                           3; Mismatches
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GAGAGGCGTTGGTTAAGGC 22
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                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                           18.6%;
73.7%;
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29-AUG-2000; 2000US-0228854P
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Best Local Similarity 73.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                   ABQ11043 standard; DNA; 24
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                                                                                                                                                                             14; Conservative
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Best Local Similarity
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                                                                                               88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 7 A; 2 C; 10 G; 6 T; 0 U; 0 Other;
                                                                                              Oligonucleotide array; adapter sequence; probe;
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                                                                  Oligonucleotide adapter/capture probe 12529
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 244; 261pp; English.
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                                                                                                                                                                                                                                     25-AUG-2000; 2000US-0227948P.
29-AUG-2000; 2000US-0228854P.
                                                                                                                                                                                                           27-AUG-2001; 2001WO-US026519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ12579 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 73.7.
                                                                                                                                                                                                                                                                              (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                     WPI; 2002-292068/33
                                                                                                                                                    WO200216649-A2
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                                                                                                                                                                                                                                                                                                           Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-2002
                                        11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2002.
                                                                                                                                                                               28-FEB-2002
                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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BXBXSXXXXX
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(SEQU-) SEQUENOM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2005014846-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ношо варіелв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOC145197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADY03184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roth RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
ADY03184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an oligonucleotide array (I) comprising at least different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABO00010-ABO13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABO00010-ABO13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                           or detecting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                   Array comprising adapter sequences useful for immobilizing or de target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.6%; Score 15.8; DB 6; Length 25; 73.7%; Pred. No. 6e+04; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reneland R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer 156 used to amplify human DPF3 SNP DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP detection; breast tumor; endocrine disease; gynecology and obstetrics; neoplasm; cytostatic; gene therapy; RNA interference; ss; PCR; primer; D4, zinc and double PHD fingers, family 3; DPF3; guanine-nucleotide exchange factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kammerer SM,
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 244; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GAGAGGGCUGGUUAAGGC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 GAGAGGCGTTGGTTAAGGC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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25-NOV-2003; 2003US-0525239P.
                        27-AUG-2001; 2001WO-US026519
                                                                        25-AUG-2000; 2000US-0227948P
29-AUG-2000; 2000US-0228854P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADY01452 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                     (ILLU-) ILLUMINA INC
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                                                                                                                                                                                                                                                     WPI; 2002-292068/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2005014846-A2
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                                                                                                                                                                                                        Gunderson K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ADY01452
LXX
AC ADX01
XX
AC ADX01
XX
DT 05-M
XX
DT 05-M
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DE PCR 7
XX
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                                                                                                                                                           of breast cancer comprising detecting the presence or absence of a polymorphic variation associated with breast cancer. The method of the invention demonstrates cytostatic activity and may be useful for identifying a risk of, preventing and/or treating breast cancer and cancer metastasis. The methods may be utilized for gene therapy or RNA interference. The current sequence is that of a PCR primer of the invention which was used to amplify a human rho-family guanine-nucleotide exchange factor D4, zinc and double PHD fingers, family 3 (DPP3) DNA containing a single nucleotide polymorphism (SNP).
                                                                                                                                           The invention relates to a novel method for identifying a subject at risk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for identifying a subject at risk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP detection; breast tumor; endocrine disease; gynecology and obstetrics; neoplasm; cytostatic; metastasis; gene therapy; RNA interference; ds; SNP; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of breast cancer comprising detecting the presence or absence of a polymorphic variation associated with breast cancer. The method of the invention demonstrates cytostatic activity and may be useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide sequences within the human genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                               18.4%; Score 15.6; DB 14; Length 30; 40.0%; Pred. No. 7.6e+04; tive 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reneland R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer 7 used to amplify human LOC145197 SNP DNA.
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30 BP; 5 A; 7 C; 7 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kammerer SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 AAGUUGGAAGGCGCUUUGCUUCUGUUUUC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACGTTGGATGGGTCACATACTTCTGTCTTC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 17; Page 296; 617pp; English.
                                                                                                 Example 16; Page 239; 617pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
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25-NOV-2003; 2003US-00723681.
25-NOV-2003; 2003US-0525239P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-2004; 2004WO-US016939.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.0
Matches 12; Conservative
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CC cancer metastasis. The methods may be utilized for gene therapy or RNA CC interference. The current sequence is that of a PCR primer of the CC interference. The current sequence is that of a PCR primer of the CC invention which was used to amplify a human LOC145197 DNA containing a XX Squence 30 BP; 5 A; 7 C; 8 G; 10 T; 0 U; 0 Other;

Query Match

Query Match

Best Local Similarity 43.3%; Pred. No. 7, 5e+04;

Matches 13; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
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Search completed: October 16, 2006, 14:15:59 Job time : 446.812 secs

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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-385230
US-10-719-900-385230
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Sequence 111, App
Sequence 11212,
Sequence 13212, A
Sequence 13212, A
Sequence 106490,
Sequence 713202,
Sequence 386034,
Sequence 386035,
Sequence 386036,
Sequence 386965,
Sequence 386965,
                                                                                                                                                                                                                                                                                                                  Published Applications NA Main:*

1: KBMC Celerra_SIDS3/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
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Sequence 70, Appl
                                                                         October 16, 2006, 14:16:09 , Search time 1197.03 Seconds (without alignments) 872.534 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 385230,
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                                                                                                                                           1 ggguuaucugcaacugagag......uuuucuggaugcagaguccu
          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-719-900-453865

US-10-933-982-172709

US-10-403-61-111

US-10-310-914A-166555

US-10-750-185-13212

US-10-750-185-13212

US-10-750-623-13212

US-10-310-914A-106490

US-10-310-914A-106490

US-11-121-849-38693

S US-11-121-849-386035

S US-11-121-849-386965

US-10-719-900-888593

US-10-719-900-888593

US-10-719-900-888593
                                                                                                                                                                                                18892170 segs, 6143817638 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    - nucleic search, using sw model
                                                                                                                                                               IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                   US-10-604-726A-6033
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Match Length DB
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Perfect score:
                                                                                                                                                                Scoring table:
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Sequence 96809, A Sequence 172712, Sequence 172720, Sequence 56788, A Sequence 310318,

Sequence 28545, A Sequence 539345, Sequence 539345, Sequence 15707, A Sequence 908282, Sequence 908626, Sequence 211873, Sequence 214920, Sequence 640087, Sequence 54286, Sequence 317240, Sequence 317240, Sequence 559311, Seque

US-10-719-956-28545
US-10-719-956-281709
US-10-719-956-411709
US-10-719-956-411709
US-10-719-956-411709
US-10-809-189-15707
3 US-11-036-317-705480
3 US-11-036-317-908282
US-11-121-849-258626
US-11-121-849-258626
US-11-121-849-258626
US-11-121-849-278380
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US-10-719-900-659931
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US-10-719-900-559931
US-10-719-914A-324009
US-10-719-914A-324009
US-10-719-914A-324009
US-10-719-914A-324009
US-10-719-914A-324009
US-10-933-982-172720

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                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 385230
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                       Sequence 385230, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT FILING DATE: 2003-11-20
FRIOR APPLICATION NUMBER: 60/427,808
FRIOR FILING DATE: 2002 11 20
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Publication No. US20050026164A1
Publication No. US20050026164A1
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REPERENCE: 3528.1
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.4%; Score 18.2; DB 9; Best Local Similarity 43.5%; Pred. No. 1.4e+04; Matches 10; Conservative 10; Mismatches 3;
ALIGNMENTS
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APPLICATY: Anderson, David et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

TITLE REFERENCE: 21402-573C

CURRENT APPLICATION NUMBER: US/10/403,161

CURRENT FILING DATE: 2003-03-31

PRIOR APPLICATION NUMBER: 60/370349

PRIOR APPLICATION NUMBER: 60/384543

PRIOR APPLICATION NUMBER: 60/384543

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2002-06-30

PRIOR PILING DATE: 2002-06-16

PRIOR PILING DATE: 2002-06-15

PRIOR APPLICATION NUMBER: 60/403748

PRIOR APPLICATION NUMBER: 60/372019

PRIOR PILING DATE: 2002-04-12

PRIOR APPLICATION NUMBER: 60/374379

PRIOR PILING DATE: 2002-04-22

PRIOR PILING DATE: 2002-04-22

PRIOR PILING DATE: 2000-04-22

PRIOR PILING DATE: 2000-04-22

PRIOR FILING DATE: 2000-02-08

PRIOR PILING DATE: 2000-02-08

PRIOR FILING DATE: 2002-01-22
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; Publication No. US20060051769A1
; Publication No. US20060051769A1
; GENERAL INPORMATION:
; APPLICANT: Barts, Jennifer
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
; FILE REFERENCE: 3700
; CURRENT APPLICATION NUMBER: US/10/933,982
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 224976
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 172709
; LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                      21.4%; Score 18.2; DB 9; Length 25; 69.6%; Pred. No. 1.4e+04;
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 453865
LENGTH: 25
                                                                                                                                                                                                                                                                                             3; Indels
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                                                                                                                                                                                                                                                                  Pred. No. 1.46
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                  35 GUCCCCAAGUUGGAAGGGCGCUU 57
                                                                                                                                                                                                                                                                                                                                                                                1 GACCCCAAGTTGGAAGGCGGCTT 23
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; Publication No. US20040043930A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-453865
                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-10-933-982-172709/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-172709
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US-10-403-161-111/c
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Sequence 166755, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Wusat
APPLICANT: Shiler, Wusat
APPLICANT: Shiler, Wusat
APPLICANT: Shiler, Wusat
APPLICANTON: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 166755
LENGTH: 27
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PRIOR APPLICATION NUMBER: 60/262892
PRIOR FILING DATE: 2001-01-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 173
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 111
LENGTH: 26
                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Description of Artifical Sequence: Primer/Probe US-10-403-161-111
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APPLICANT: BAIES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIL1100-2
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 13122
LENGTH: 24
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21.4%; Score 18.2; DB 8;
Best Local Similarity 65.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 5; Mismatches 3;
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: BENOMICS, Sue K.
APPLICANT: RERK Richard
APPLICANT: RESERVELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CUGCAACUGAGAGGGGCUGGUUA 30
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                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 43.5*
Matches 10; Conservative
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US-10-310-914A-166755/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-750-185-13212
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| Sequence 292693 | Sequence 292693 | Sequence 292693 | Sequence 292693 | Application US/11121849 | Sequence 292693 | Application No. US20050272080A1 | Sequence 292693 | Application No. US20050272080A1 | Sequence 292693 | Application No. US20050272080A1 | APPLICANT: John Palma | TITLE OF INVENTION: Microarrays | TITLE OF INVENTION: Microarrays | FILE OF INVENTION: MICROARRAY | SOGN-10 | CURRENT APPLICATION NUMBER: US/11/121,849 | CURRENT APPLICATION NUMBER: 00/567,949 | PRIOR APPLICATION NUMBER: 00/567,949 | PRIOR APPLICATION NUMBER: 00/567,949 | PRIOR ELLING DATE: 2004-05-03 | NUMBER OF SEQ ID NOS: 673904 | SOGNTWARE: Microarray Probe Sequence Listing Generator V 1.1 | SEQ ID NO 292693 | LENGTH: 25
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                                                                                                                                                                                                                                                                                                             Sequence 713202, Application US/11036317

| Sequence 713202, Application US/11036317
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
| APPLICANT: Blume, John
| TITLE OF INVESTION: Method of Analysis of Alternative Splicing in Mouse:
| TILE REFERENCE: 3654.1
| CURRENT APPLICATION NUMBER: US/11/036,317
| CURRENT FILING DATE: 2005-01-13
| PRIOR APPLICATION NUMBER: US 60/536,639
| PRIOR APPLICATION NUMBER: US 60/536,639
| PRIOR PILING DATE: 2004-01-13
| NUMBER OF SEQ ID NOS: 991174
| SEQ ID NO 713202
| LENGTH: 25
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66.7%; Pred. No. 2.3e+04;
tive 4; Mismatches 4;
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41.7%; Pred. No. 2.3e+04;
iive 10; Mismatches 4;
Best Local Similarity 45.8%; Pred. No. 2.3e+04; Matches 11; Conservative 9; Mismatches 4
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                                                                                                50 GGGCGCUUUGCUCUGUUUCUGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 GAGAGGGCUGGUUAAGGCGUCCC 39
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1 CTATGCTTAGATTTTCTGGATGCA
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Best Local Similarity 41...
Best Local Similarity 41...
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Best Local Similarity 66.7
Matches 16; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-713202
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; ORGANISM: Homo sapien
US-11-121-849-292693
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US-11-121-849-386034/c
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i Sequence 106490, Application US/10310914A

i Sequence 106490, Application US/10310914A

j Publication No. US20060003322A1

GENERAL INPORMATION: Beac

j APPLICANT: Bhiler, Kvuzat

j APPLICANT: Bhiler, Kvuzat

j TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

TITLE OF INVENTION: Uses thereof

CURRENT APPLICATION UNMERR: US/10/310, 914A

CURRENT APPLICATION UNMERR: US/10/310, 914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 106490

LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13212, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
APPLICANT: MINION: MIN
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2e+04;
ches 2;
                                                                                                                                                                                                Query Match 20.9%; Score 17.8; DB 10;
Best Local Similarity 38.1%; Pred. No. 2e+04;
Matches 8; Conservative 11; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
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Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PAtentIN version 3.1
                                                                                                                                                                                                                                                                                                                                  56 unuccuncucumucuceaug 76
                                                                                                                                                                                                                                                                                                                                                                        1 TTTACATCTGTTTTCTGGATG 21
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                                                                    ; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-13212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Reverse Primer US-10-750-623-13212
TYPE: DNA
ORGANISM: Artificial sequence
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38.1%;
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LENGTH: 24
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RESULT 14

US-11-121-089-386866/c

US-11-121-080-066, Application US/11121849

Sequence 386966, Application US/11121849

Publication No. US2000272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

TITLE OF INVENTION: Microarrays

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2004-05-03

PRIOR PILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Publication No. US20060003322A1

GENERAL INFORMATION:
GENERAL SAPILICANT:
FILE OF INVENTION:
USGS (DESCOINGED)
FILE OF INVENTION:
USGS (DESCOINGED)
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 776242
LENGTH: 24
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                                                                Score 17.6; DB 15;
Pred. No. 2.3e+04;
5; Mismatches 4;
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                                                                                                                                                                 8 CUGCAACUGAGAGGGGCUGGUUAA 31
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                                                                     Query Match 20.7%;
Best Local Similarity 62.5%;
Matches 15; Conservative
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ORGANISM: Homo sapien
    ; ORGANISM: Homo sapien
US-11-121-849-386965
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US-10-310-914A-776242/c
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US-10-310-914A-776242
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US-11-121-849-386035/C
US-11-121-849-386035/C

SQUENCE 386035, Application US/11121849

Publication No. US2000272080A1

GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STILE REFERENCE: 3684.1

CURRENT APPLICATION WUMBER: US/11/121,849

CURRENT APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SEQ ID NOS: 673904

LENGTH: 25

LENGTH: 25
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US-11-121-849-386965/C
is Sequence 386965, Application US/11121849
is Publication No. US20050272080A1
is GENERAL INFORMATION:
is APPLICATION Balma
is TITLE OF INVENTION: Microarray8
if TITLE OF INVENTION: Microarray8
is FILE REFERENCE: 3684.1
is FILE REFERENCE: 3684.1
is FURENT APPLICATION NUMBER: US/11/121,849
is CURRENT FILING DATE: 2005-05-03
is PRIOR PILING DATE: 2004-05-03
is NUMBER OF SEQ ID NOS: 673904
is SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
is LENGTH: 25
it TYPE: DNA
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR PLICATION NUMBER: 05/567,949
PRIOR PLICATION PROBER: 2006-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: McCroarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 386034
LENGTH: 25
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Pred. No. 2.3e+04;
5; Mismatches 4;
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Local Similarity 62.5%;
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US-11-121-849-386035
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Matches 15; Conser
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Best Local S:
Matches 15
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Sequence 17, Appl
                                                                                  October 16, 2006, 14:16:55; Search time 188.534 Seconds (without alignments) 842.395 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                    / RMC Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/ RMC Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ RMC Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ RMC Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ RMC Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/ RMC Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/ RMC Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-217-529-96809
US-11-348-413-966036
US-11-217-529-52650
US-11-217-529-98397
US-11-217-529-98397
US-11-217-529-9848
US-11-217-529-9848
US-11-217-529-9848
US-11-348-413-414079
US-11-348-413-414079
US-11-348-413-884139
US-11-348-413-884139
US-11-348-413-988157
US-11-348-413-988357
US-11-348-413-988357
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US-11-348-413-988357
US-11-348-413-411717
US-11-348-413-411717
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                                                                                                                                                                                                                                                       2395520 seqs, 934235491 residues
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Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length
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Perfect score:
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16.4
16.2
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Sequence 9396, Ap Sequence 73247, A Sequence 137108, Sequence 152213,		Sequence 988355, Sequence 988355, Sequence 1137776, Sequence 173043, Sequence 170826,	1486
US-11-217-529-9396 US-11-217-529-73247 US-11-217-529-137108 US-11-217-529-152213	US-11-217-529-192382 US-11-348-413-245155 US-11-348-413-361458 US-11-348-413-669513 US-11-348-413-671197 US-11-348-413-858122 US-11-348-413-957263	US-11-348-413-984936 US-11-348-413-988355 US-11-348-413-988356 US-11-348-413-1137776 US-11-217-529-173043 US-11-348-413-170826 US-11-348-413-170826	
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ALIGNMENTS

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Sequence 835989, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wurphy, Bllen
APPLICANT: Olmsted, Stephen
APPLIC
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40.0%; Pred. No. 6.3e+03;
iive 10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/USOS/035471
PRIOR FILING DATE: 2005-10-05
PRIOR PRIOR OF PROPERIOR NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 035980
LENGTH: 25
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Matches 10; Conservative
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NAME/KEY: misc_feature
LOCATION: (1)..(25)
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US-11-348-413-835988
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RESULT 2 US-11-217-529-96809/c ; Sequence 96809, Application US/11217529 ; Publication No. US20060099612A1

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TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR PELICATION NUMBER: PCT/USO5/035471
PRIOR PELICATION NUMBER: US 11/243,445
PRIOR PELICATION NUMBER: US 60/615,573
PRIOR PELICATION NUMBER: US 60/615,573
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR APPLICATION NUMBER: US 60/615,573
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 96036
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
SORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(25)
COTHER INFORMATION: SEQ ID NO: 10014; WANOIPG3J_at; Start 207; Stop 231;
UCTHER INFORMATION: 00000000100000
US-11-348-413-960036
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APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NOBAMA, YUKKO
APPLICANT: FUJIMIRA, NORIHISA
APPLICANT: FUJIMIRA, TOMOKO
APPLICANT: FUJIMIRA, TOMOKO
APPLICANT: FUJIMIRA, TOMOKO
APPLICANT: FUJIMIRA, TOMOKO
APPLICANT: FUJIMIRA, 109HIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217, 529
CURRENT FILING DATE: 2005-09-02
PRIOR FILING DATE: 2004-09-02
PRIOR FILING DATE: 2004-09-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.1%; Score 16.2; DB 9; 33.3%; Pred. No. 1.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 52650, Application US/11217529
; Publication No. US20060099612A1
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SOFTWARE: Patentin version 3.3
SEQ ID NO 52650
LENGTH: 25
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Best Local Similarity 33.3%
Matches 7; Conservative
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Matches 15; Conserv
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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: RUJIMURA, TONKINO
; APPLICANT: FUJIMURA, TONKINO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REPERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT PILING DATE: 2005-09-02
; PRIOR FILING DATE: 2005-09-02
; PRIOR PELLING DATE: 2005-09-02
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                                                                                        APPLICANT: NAKAMURA, NORIHISA
APPLICANT: NORAMURA, NUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: KUJAMIRA, TOMOKO
APPLICANT: ASHIKAN, TOMOKO
APPLICANT: ASHIKAN, TOMOKO
APPLICANT: ASHIKAN, TOMOKO
APPLICANT: ASHIKAN, TOMOKO
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
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19.5%; Score 16.6; DB 8; Length 25;
Best Local Similarity 60.9%; Pred. No. 8.9e+03;
Matches 14; Conservative 5; Mismatches 4; Indels
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19.3%; Score 16.4; DB 8; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 9; Conservative 8; Mismatches 1; Indels
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Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 UCCCCAAGUUGGAAGGGCGCUUU 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Saccharomyces pastorianus US-11-217-529-96809
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24 TICCCAATIGIGAAGGGCGCTII 2
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SOFTWARE: Patentin version 3.3
SEQ ID NO 96809
LENGTH: 25
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SOFTWARE: PatentIn version 3.3
                                            APPLICANT: SUNTORY LIMITED APPLICANT: NAKAO, YOSHIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-11-348-413-960036/c
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LENGTH: 25
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Sequence 411718, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-99137
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Best Local Similarity
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US-11-217-529-29948/C
US-11-217-529-29948/C
Sequence 29948, Application US/11217529
Fublication No. US2006009612A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAWURA, NORTHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
TITLE OF INVENTION: METHOUS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
TITLE OF INVENTION: METHOUS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2004-09-02
PRIOR FILING DATE: 2004-09-02
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAWURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIWURA, TOWKO
APPLICANT: RUNENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
FRIOR APPLICATION NUMBER: US 10/932,182
PRIOR PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 127023
SOFTMARE: PATENTIN OFFICIAL OFFICE OF TOWNS: 127023
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18.4%; Score 15.6; DB 8;
Best Local Similarity 45.5%; Pred. No. 2.1e+04;
Matches 10; Conservative 8; Mismatches 4;
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APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAOWRA, NORIHISA
APPLICANT: KODAWA, YUKIKO
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIWURA, TOWOKO
APPLICANT: ASHIKARI, TOSHIHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Saccharomyces pastorianus US-11-217-529-29948
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GCTTTGCTTCTGGTTTATG 22
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SOFTWARE: Patentin version 3.3
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Best Local Similarity 36.0.
Best Local 7; Conservative
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LENGTH: 25
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LENGTH: 25
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APPLICANT: Mounte, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
AITILE OF INTERCHION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
PRIOR APPLICATION NUMBER: PCT/USO5/035471
PRIOR APPLICATION NUMBER: US/12/34445
PRIOR PLING DATE: 2005-10-05
PRIOR PAPLICATION NUMBER: US 11/243,445
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Publication No. US20060099612A1

GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAWIRA, NORIHISA

APPLICANT: NAKAWIRA, YUKIKO

APPLICANT: KODAMA, YUKIKO

APPLICANT: KODAMA, YUKIKO

APPLICANT: TOSHIHIKO

TITLE OF INVENTION: METHIOS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: S-38-285

CURRENT APPLICATION NUMBER: US/11/217,529

CURRENT APPLICATION NUMBER: US 10/932,182

PRIOR APPLICATION NUMBER: US 10/932,182

PRIOR APPLICATION NUMBER: US 10/932,182

PRIOR FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 197023

SEQ ID NO 99137

LENGTH: 25
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TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217, 529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 94477
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches
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APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US/11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
RIOR FILING DATE: 2004-10-05
RIOR FILING DATE: 2004-10-05
SEQ ID NOS: 1276209
SEQ ID NOS: 1276209
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APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
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LOCATIONS (1): (25)
OTHER INDORANTION: SEQ ID NO: 7816; WANOIUMPL_at; Start 185; Stop 209;
OTHER INFORMATION: 000000010000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(25)
COCTHER INFORMATION: SEQ ID NO: 12552; WANOIUOO2; Start 495; Stop 519;
OTHER INFORMATION: 000000000011111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 18.4%; Score 15.6; DB 9; Similarity 36.4%; Pred. No. 2.1e+04; 8; Conservative 10; Mismatches 4;
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CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILLING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR PLING DATE: 2004-10-05
SEQ ID NO 884139
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; Sequence 884139, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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                    Mounts, William M
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Best Local Similarity 36.4<sup>†</sup>
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: probe
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Best Local Similarity
Matches 8; Conserva
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APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (Am 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: US/11/243,445
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR APPLICATION NUMBER: US 01/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2005-10-05
PRIOR PILING DATE: 2004-10-05
SEQ ID NOS: 1276209
SEQ ID NO 414079
TYDE: 25
TYDE: 25
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                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: SEQ ID NO: 12488; WAN01UOM6; Start 38; Stop
; OTHER INFORMATION: 00000000011110
US-11-348-413-411718
                                                                                                                                                                                                                                                                                                                                                                                Length 25;
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Best Local Similarity 36.4%; Pred. No. 2.1e+04;
Matches 8; Conservative 10; Μίπματτήρα
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PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 411718
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 GCUUUGCUUCUGUUUUCUGGAU 75
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                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 36.41
Matches 8; Conservative
                                                                                                                                                                                                  OTHER INFORMATION: probe
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                                                                                                                                                        ORGANISM: Artificial
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US-11-348-413-414080/c
                                                                                                                                      TYPE: DNA
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAORA, YOSHIHIRO
APPLICANT: NAKAORA, YOSHIHIRA
APPLICANT: NAKANTRA, NORIHISA
APPLICANT: FUJINURA, TOMOKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SOFTWARE: 25
LENGTH: 25
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| LOCATION: (1). (25)
| OTHER INFORMATION: SEQ ID NO: 10828; WAN01UOXH; Start 36; Stop 60;
| OTHER INFORMATION: 00000000011101
| US-11-348-413-350690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.1%; Score 15.4; DB 8; Length 25; Best Local Similarity 52.0%; Pred. No. 2.5e+04; Matches 13; Conservative 6; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 CUUCUGUUUUCUGGAUGCAGAGUCC 84
                                                                                                                       Sequence 98618, Application US/11217529; Publication No. US20060099612A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::| ::| ||| ||| ||| ||| 25 CTTCAAAATTCTGGACGCAGGGAGGTGTCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Saccharomyces pastorianus US-11-217-529-98618
54 gcuungcuncuguuucuggau 75
                 25 GATTGGCCTCTGTTTTCTTGAT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: probe
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US-11-348-413-350690/c
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   Length 25;
                                     Indels
 18.1%; Score 15.4; DB 9; ilarity 40.0%; Pred. No. 2.5e+04; Conservative 9; Mismatches 6;
Query Match
Best Local Similarity
Matches 10; Conserv
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Search completed: October 16, 2006, 14:22:02 Job time: 189.534 secs

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AC141634 CACNAID B
AC141632 CACNAID t
AC141636 CACNAID E
AC143064 CACNAID B
AC657579 Human ost
AD679069 Rat ZAQ r
AD150688 Rat G pro
Ad65918 And iogene
Aas95201 Ottoferlin
Aca55301 Anti-myos
Ac29113 Human PDE
Abd32144 Human PDE
Abd32144 Human PDE
Abd32144 Human PDE
Abd3214252 Antienne
Ad44052 Antienne
Ad44052 Antienne
Ad413368 Human BNA
Ad44508 Knock-dow
Ac61039 Human mic
Ac41039 Human deb

nucleic

Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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The invention relates to an oligonucleotide array (1) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (1) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid correct acid correct acid correct acid correct acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Array comprising adapter sequences useful for immobilizing or detecting target nucleic acid sequence, has different addresses comprising different specific capture probes.
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                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide array; adapter sequence; probe;
                                                                                                                                                                                                                                                                                                                                             Oligonucleotide adapter/capture probe 10993
                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                     ADD64634
ADO61007
AEC90171
ADZ15690
ADZ15691
ADW95301
AAQ89038
ACL41634
ACL41632
ACL43064
AED57579
                                                 ADD69148
AAS95201
AEA25301
AEA25458
ABZ99113
ABD32144
ADJ60998
                                                                                                            ADO46487
ADZ97886
AED42052
ADJ13385
ADU43508
AAF85432
ACK10389
                                 ABQ79069
ABL50688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 225; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2001; 2001WO-US026519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-AUG-2000; 2000US-0227948P.
29-AUG-2000; 2000US-0228854P.
 ABQ11002 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-292068/33.
WO200216649-A2
                                                                                                                                                                                                                                                                                                                             11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
ABQ11002;
                                                                                                                                                                                                                                                                                     ABQ11002
 RESULT
                                                                             0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Abg00358 Oligonucl
Abg11043 Oligonucl
Abg12538 Oligonucl
Abg12579 Oligonucl
Aar74315 PCR prime
Aar360117 Human CAB
Ada24254 Major all
Ada27865 Human ant
Adj13347 Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ada61591 Human Tes
Ad18277 Human mic
Acd57816 HCV DNAzy
Ad183268 HCV DNAzy
Aac47817 PCR prime
Aax04299 Mouse neu
                                                          ; Search time 125.594 Seconds (without alignments) 1332.341 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abq11002 Oligonucl
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
         GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                        4443654
                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                      5244920 seqs, 3486124231 residues
                                                                                                             24
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                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ04674
ABQ04115
ABQ00158
ABQ11043
ABQ12238
ABQ12279
AAT74115
AAL50117
ADZ27868
ADZ27864
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ACI82777
ACD57816
ADI83268
AAT47817
AAX04299
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                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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geneseqn2001bs:*
geneseqn2001bs:*
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Match
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Perfect score:
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Result

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The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
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Pred. No. 1.3e+03;
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                                                                                                                                                                             Oligonucleotide array; adapter sequence; probe;
                                                                                                                                   Oligonucleotide adapter/capture probe 4706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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2000US-0228854P.
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73.7%;
  ABQ04715 standard; DNA; 24
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les 14; Conservative
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29-AUG-2000;
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                                                                                                                                                                                                                         Synthetic.
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                                              ABQ04715;
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Matches
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and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                               Gaps
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                                                                                                                               Query Match 65.8%; Score 15.8; DB 6; Length 24; Best Local Similarity 73.7%; Pred. No. 1.3e+03; Matches 14; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide array; adapter sequence; probe; ss.
                                                                                       Sequence 24 BP; 7 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide adapter/capture probe 4665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              target nucleic acid sequence, has different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 147; 261pp; English
                                                                                                                                                                                                                         2 GAGAGGGCUGGUUAAGGC 20
                                                                                                                                                                                                                                                                   4 GAGAGGCGTTGGTTAAGGC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GAGAGGGCUGGUUAAGGC 20
                                                                                                                                                                                                                                                                                                                                                                                ABQ04674 standard; DNA; 24 BP
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29-AUG-2000; 2000US-0228854P
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                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ04674;
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Oligonucleotide array; adapter sequence; probe; ss.
                                    Oligonucleotide adapter/capture probe 349
                                                                                                           27-AUG-2001; 2001WO-US026519.
                                                                              WO200216649-A2
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RESULT 3 ABQ04715/c

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Gaps

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2; Indels

24;

Gaps

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Indels

24;

Length

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25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) a useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
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target nucleic acid sequence, has different addresses comprising
different specific capture probes.
                                                                                                                                                                                                                                                                                     Seguence 24 BP; 5 A; 10 C; 2 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 6;
Pred. No. 1.3e+03;
3; Mismatches 2;
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Pred. No. 1.3e+03;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide array; adapter sequence; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide adapter/capture probe 12529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GAGAGGGCUGGUUAAGGC 20
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29-AUG-2000; 2000US-0228854P.
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Best Local Similarity 73.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                           Query Match 65.8%;
Best Local Similarity 73.7%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide adapter/capture probe 11034
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                                         25-AUG-2000; 2000US-0227948P
29-AUG-2000; 2000US-0228854P
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29-AUG-2000; 2000US-0228854P
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                                                                                                                                  (ILLU-) ILLUMINA INC
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Gaps

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Indels

Length 25;

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Corynascus heterothallicus.
                                                                                       29-JAN-1996;
                                                                    29-JAN-1997;
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                           WO9728243-A1
                                                07-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleaning; bleaching; cellulose; fabric; enzyme hybrid; peroxidase; cellulose binding domain; Humicola insolens; cellulase; Coprinus cinereus; laccase; plasmid pJC25; PCR; primer; ss.
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                                                                                                                                  Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 5 A; 10 C; 2 G; 8 T; 0 U; 0 Other;
                                                                                                             Oligonucleotide adapter/capture probe 12570.
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5 GAGAGGCGTTGGTTAAGGC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 GAGAGGGTTGGTTAAGGC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                    25-AUG-2000; 2000US-0227948P.
29-AUG-2000; 2000US-0228854P.
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                                                 ABQ12579 standard; DNA; 25
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                                                                                         11-JUN-2002 (first entry)
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                                                                                                                                                                         WO200216649-A2
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                                                                                                                                                                                            28-FEB-2002
                                                                                                                                                      Synthetic.
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PCR primers CiPpcrdwn (AAT74310) and JC25.2 (AAT74315) were used to amplify a DNA fragment encoding the entire laccase protein (residues 1-620) of Myceliophthora thermophila plus 232 bp of upstream sequence, using plasmid pJRoC30 as template. The PCR product was ligated to a DNA fragment encoding the Humicola insolens family 45 cellulase linker domain (35 amino acids), the H. insolens family 45 cellulase cellulose binding domain (CBD, 37 amino acids) plus 20 bp of 3'-noncoding sequences in vector pJC106 to obtain plasmid pJC25 (see AAT74282). A claimed process for removal or bleaching of soiling or stains on a cellulosic fabric comprises contacting the fabric with a modified enzyme fibrid comprising a catalytically active portion of a non-cellulolytic enzyme linked to a CBD. The hybrid enzyme gives improved enzyme performance by increasing the affinity of the enzyme for the fabric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; CAB55953.1; nuclear hormone receptor ligand binding domain; LBDG3; cancer; autoimmune disorder; inflammation; PCR; antiseborrheic; dermatological; anti-HIV; neuroprotective; nephrotropic; antianginal; transquilizer; antiarrhythmic; antiarreriosclerotic; antiasthmatic; cardiant; antidepressant; antidiabetic; vasotropic; antinflammatory; nephrotropic; cytostatic; antilipemic; hypotensive; antinflammatory; antithyroid; antilipemic; hypotensive; antiallergic; cerebroprotective; nephrotropic; antilipemic; hypotensive; antiallergic; cerebroprotective; haemostatic; thrombolytic; cardiovascular disorder; neurological disorder; infection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Cleaning of cellulosic fabrics - using an enzyme hybrid comprising sequence of a non-cellulolytic enzyme linked to a cellulose-binding
                                                                                                                                                                                                                                                  Rasmussen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.3%; Score 15.2; DB 2; Length 28; 75.0%; Pred. No. 2.5e+03; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CAB55953-1 ligand binding domain PCR primer #2.
                                                                                                                                                                                                                                                  Vind J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 BP; 3 A; 15 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                  Von Der Osten C, Cherry JR, Bjornvad M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 85; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GAGAGGGCUGGUUAAGGCG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GCGAGTGGCTGGTCAAGGCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL50117 standard; DNA; 24 BP
97WO-DK000042.
                                                                                      96DK-00000094
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nes 15; Conservative
                                                                                                                                                                    (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                    WPI; 1997-402598/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200270557-A2
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The present invention describes a method for testing the presence or absence of a specific substance in a food by performing PCR with primers which are designed on the basis of data obtained from a part of a gene of the specific substance. Also described: (1) a similar method for detecting a trace component contained in a food, or for identifying a harmful allergen specific to a consumer of such substance by performing PCR with primers which are designed on the basis of data obtained from a part of a gene of the specific substance; (2) primers for PCR applicable in food testing which are designed on the basis of data obtained from a part of a gene of the specific substance; and (3) kits for determining concentration of a specific substance in the food containing the primers. The methods are useful for testing foods, which can be used in detecting trace components or identifying specific harmful allergens in (processed) foods, particularly applicable in food safety and management. The present allergenic storage protein designated FAGAGI, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                             PCR-based method for testing foods using specific primers designed from genes of target substance, useful in detecting trace components or identifying specific harmful allergens in (processed) foods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.0%; Score 14.4; DB 9; 68.8%; Pred. No. 5.9e+03;
                                                                                                                                                                                          Suzuki E, Miyatake K, Hayakawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein interaction; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human antisense oligonucleotide SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 10; 38pp; Japanese.
                                                                                                                            (NISS ) NISSHIN SEIFUN GROUP INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0256986P.
2001US-0259571P.
2001US-0259572P.
   26-SEP-2002; 2002WO-JP009982.
                                                                 15-FEB-2002; 2002JP-00038930.
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2000US-0185056P.
2000US-00727384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GGGCTGGTTATGGCGT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADZ97885/c
ID ADZ97885 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 68.8 les 11, Conservative
                                                                                                                                                                                                                                                  WPI; 2003-637145/60.
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04-JAN-2001; 2
04-JAN-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999;
                                                                                                                                                                                       famakawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ97885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
   #X#X#X#X#X#####X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HANDER BERKER BERKER SERVER SERVER BERKER BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thusan nuclear hormone receptor legand binding domain designated cancer, autoinmune/inflammatory disorders, including allergy, inflammatory bowel disease, arthritis, psoriasis and respiratory tract inflammatory bowel disease, arthritis, psoriasis and respiratory tract inflammatory bowel of the cardiovascular disorders, including and organ transplant rejection, cardiovascular disorders, including comparation, oedema, angina, atherosclerosis, thrombosis, sepsis, shock, reperfusion injury, heart arrhythmia, and ischaemia, neurological disorders including central nervous system disease, Alzheimer's disease, brain injury, stroke, amyotrophic lateral sclerosis, anxiety, depression and pain, developmental disorders, metabolic disorders including diabetes mellitus, osteoporosis, lipid metabolism disorders, hyperthyroidism, hypercalcaemia, hypercholesterolaemia, hypercholesterolaemia, hypercalcaemia, hypercholesterolaemia, disorders including acne, eczema and wound healing, negative effects of aging, acquired immunodeficiency syndrome (AIDS), viral, bacterial, fungal and acquired immunodeficiency syndrome (AIDS), viral, bacterial, fungal and those in which nuclear hormone receptors are implicated. The present sequence is a PCR primer used to isolate the coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                         New CAB55953.1 or LBDG3 polypeptide, useful as a nuclear hormone receptor ligand-binding domain, or for manufacturing of a medicament for diagnosing or treating cell proliferative disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the protein and coding sequences of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                  Allen JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Major allergenic storage protein FAGAG1 PCR primer FAG19 SEQ ID NO:7.
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                                                                                                                                                                                                                                                  Pierron VN, Allen KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         food testing; allergen; PCR primer; Fagopyrum esculentum;
major allergenic storage protein; FAGAG1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                  Phillips T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 64; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune/inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AGAGGGCUGGUUAAGGCGUC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 AGAGGGCTTATTAACTCGTC 3
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                                                              05-MAR-2002; 2002WO-GB000937
                                                                                                                            05-MAR-2001; 2001GB-00005402
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                                                                                                                                                                                    (INPH-) INPHARMATICA LTD
                                                                                                                                                                                                                                                     Phelps CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fagopyrum esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              WPI; 2002-698731/75
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12-SEP-2002.
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                                                                                                                                                                                                                                                                                   Potter SJ;
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                                                                                                                                                                                                                                                     Fagan RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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Gaps

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88.

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Length 21; 1; Indels

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WO200026352-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                             invention
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          (GARN/)
(MINN/)
(LUEB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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  g
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                                                                                                                                                                                                                                                                   The invention relates to a method for modulating, in a host cell, a protein-protein interaction between a first protein which is PRAK (P18-cryquated/activated protein kinase or MAPKAPKS) and a second protein which is BRAS (extracellular signal-regulated kinase 3). The method comprises administering to the cell a compound capable of modulating the protein-protein interaction. The method is useful in modulating in a host comprises administering in the method is useful in modulating in a host can a second protein which is BRAS or treating inflammation or inflammatory disorders, e.g., asthma, rheumatoid arthritis, juvenile chronic arthritis, myositis, Crohn's disease, gastritis, colitis, unflammatory bowel disease, proctitis, pelvic inflammatory disease, systemic luque erythematosus, rhinitis, conjunctivitis, soleritis, chronic inflammatory polyneuropathy, Tertiary conjunctivitis, psoleritis, chronic inflammatory polyneuropathy, Tertiary Lyme disease, psoriasis, dermatitis or eczema. In the exemplification of the present invention examples of antisense oligonucleotides specific to nucleic acids encoding individual proteins in tables I to 82 are provided in SEQ ID NOS:11-223 (ADZ998069).
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                                                                                                                                                                                                Modulating, in a host cell, a protein-protein interaction between first protein, PRAK, (MAPKAPKS) and second protein, ERK3, (extracellular signal-regulated kinase 3) by administering modulating compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe; 88; chemical modification; methylation; array; CpG island;
tumour suppressor; p16; human; H69; H1618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA probe used to immobilise CpG methylated DNA SeqID 474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 14.2; DB 14; Length 20; 68.4%; Pred. No. 7.3e+03; ive 3; Mismatches 3; Indels (
                                                                                                                                                   Bush A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 4 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                   Mauck K,
                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 39; 296pp; English
                                                                                                                                                   Bartel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGCCUGGUUAAGCCGUC 23
15-MAR-2001; 2001US-0276179P.
19-MAR-2001; 2001US-0277013P.
23-JUL-2011; 2001US-0307233P.
14-DEC-2001; 2001US-00014814.
21-DEC-2001; 2001US-00035343.
04-JAN-2002; 2002US-00035344.
14-MAR-2002; 2002US-00095924.
18-MAR-2002; 2002US-00095934.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2001; 2001US-0301370P
                                                                                                                          MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ13347 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 68.4 tes 13, Conservative
                                                                                                                                                   Heichman K,
                                                                                                                                                                           WPI; 2005-371623/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2003
                                                                                                                                                   Cimbora D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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This invention relates to a novel method for analysing chemically modified macromolecules. Specifically, it refers to a high throughput method for the parallel analysis of many potential sites of chemical modification (e.g. methylation) in DNA. The present invention describes treating the DNA with one or more chemical reagents that result in different base sequences depending upon the presence or absence of the modification of interest. Accordingly, a device comprising an array of probes is provided to hybridise with and select the altered DNA sequences that comprise the modifications of interest such as a CpG island. In particular, this invention refers to analysing the methylation pattern of a region of the promoter for the tumour suppressor gene p16 from two human lung tumour cell lines H69 and H1618. This oligonucleotide sequence is a human DNA probe used to immobilise CpG methylated DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                          Analysis of chemical modification of DNA involves obtaining sample of DNA to be analyzed, treating DNA with chemical reagents that result in different base sequences, and determining sequence of resulting DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Tespec PRO-3; testis specific serine protease; differentiation; trypsin family serine protease; mature testis; sperm differentiation; sperm maturation; male infertility; sterility; reproductive disorder; contraception; rapid amplification of cDNA ends; RACE PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 6 A; 11 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Tespec PRO-3 5' RACE PCR primer, hPRO3-D.
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                                                                                                                                                                                  Balog RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 474; 210pp; English
                                                                                                                                                                                  Luebke KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 UGAGAGGGCUGGUUAAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 TGAGGGTGCTGGTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP006111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 63.2
nes 12; Conservative
                                                                                                                                                                                      Garner HR, Minna JD,
                                  (MINN/) MINNA J D.
(LUEB/) LUEBKE K J.
(BALO/) BALOG R P.
                                                                                                                                                                                                                                                                WPI; 2003-874843/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365604/31
GARNER H R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Senoo C, Numata M;
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proteases (Tespec PRO; ARB01156_MBO1100) and to coDNAs encoding them (AAA5158-AG1562). It also encompasses expression vectors and host cells comprising a nucleotide sequence encoding a protease of the invention, inhibitors of the proteases and antibodies against the proteases. The novel proteases are members of the trypsin family of serine proteases, having the serine and histidine active site signatures characteristic of this family. The proteases are specifically expressed in mature testis and participate in the differentiation and maturation of sperm. The proteases are potentially useful for the development of pharmaceuticals for the treatment of male infertility and other male reproductive disorders, and for the development of contraceptives. They may also be used as reagents for the diagnosis of male infertility. Sequences

AAA61590-A61593 represent RACE (rapid amplification of cDNA ends) PCR primers used in the isolation of cDNA encoding human Tespec PRO-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Trypsin family serine proteases expressed specifically in mature testis for development of methods for diagnosis and treatment of sterility and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                     The invention relates to novel murine and human testis specific serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; probe; expressed sequence tag; microarray; gene expression;
ic variation; biallelic marker; polymorphism; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.2; DB 3; Length 25;
Pred. No. 7.4e+03;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human microarray DNA oligonucleotide SEQ ID NO 82768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 4 A; 2 C; 10 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 82768; 9pp; English.
                                                                              Example 9; Page 45; 121pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GAGGGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GATGGGCTAGTTAAGTCGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACI82777 standard; DNA; 25 BP
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Best Local Similarity 63.2%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2001; 2001US-0276759P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-567953/53.
                                       for contraception.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003104410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ното варіеля
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compounds. The array is used in monitoring gene expression levels by hybridisation to a DNA library, an analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of expension of analysis comprises to at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises the hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the corposis useful in situ hybridisation, in Southern, Northern or dotor probes is useful in in situ hybridisation, in Southern, Northern or dotor probes is useful in in situ hybridisation, sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening segments of DNA that have been for additional subclones containing segments of DNA that have been concluded and previously sequenced. The sequence presented is one of the concluder acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecule, Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amberzyme, G-cleaver ribozyme, decoy molecule, aptamer,
HBV reverse transcriptase; Enhancer I region, viral replication;
degenerative, disease state; HBV infection; HCV infection; cirrhosis;
liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
virucide; antiinflammatory; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.3%; Score 14; DB 9; Length 25; 59.1%; Pred. No. 9.2e+03; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 6 A; 4 C; 10 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAGAGGGCUGGUUAAGGCGUC 23
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08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0337659P.
05-DEC-2001; 2001US-0337055P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-2003 (first entry)
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MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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DRAPER K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PAVC/)
(LEEP/)
(DRAP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIBO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
ACD57816/c
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Blatt L, Macejak D,
Draper K, Roberts E;
          WPI; 2003-229207/22
(ROBE/) ROBERTS E.
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Mcswiggen J, Morrissey D, Pavco P, Lee P;

Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.

Claim 1; Page 243; 387pp; English.

The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNN. The nucleic acid molecules include antisense and enzymetic nucleic acids such as hammerhead ribozymes, DNAzymes, inczymes, zinzymes, amberzymes, and G-cleaver ribozymes. DNAzymes, care nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well care nucleic acid decoy molecules and gatemars that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV CC as oligonucleotides that specifically bind the Enhancer I region of HBV CC genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds and compounds and/or potential therapies directed against HBV, and compounds and compounds and/or potential therapies directed against HBV, and compounds and disease states related to HBV and HCV infection, replication and gene carenoma. The present sequence represents a substrate for one of the HCV invention are ninus strand DNAzyme sequences disclosed in the present

Sequence 17 BP; 4 A; 9 C; 1 G; 0 T; 3 U; 0 Other;

Gaps ö Query Match

S7.5%; Score 13.8; DB 8; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.1e+04;
Matches 12; Conservative 3; Mismatches 2; Indels

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6 GGGCUGGUUAAGGCGU 22

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17 GGGCAGGTTAAGGTGT 1

Search completed: October 16, 2006, 14:15:57 Job time : 128.594 secs

OM nucleic

Run on:

Sequence:

Searched:

Database

Result Š

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PAT 03-JUL-2002
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CS102090 Sequence
ARC40243 Sequence
ARI50048 Sequence
ARI50048 Sequence
ARI50043 Sequence
AR27916 ARI5608
AR42443 Sequence
AR213127 Sequence
CS02086 Sequence
AR404657 Sequence
AR404657 Sequence
AR404657 Sequence
AR534679 Sequence
AR139847 Sequence
AR13984 Sequence
AR13984 Sequence
AR13984 Sequence
AR13984 Sequence
AR137924 Sequence
AR3924 Sequence
AR3924 Sequence
AR3924 Sequence
AR3924 Sequence
AR3924 Sequence
AR34255 Sequence
AR34255 Sequence
AR234255 Sequence
AR234255 Sequence
AR234255 Sequence
AR23425 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity 73.7%; Pred. No. 6.2e+04;
Matches 14; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 bp DNA Sequence 4341 from Patent WO0216649. AX447886 AX447886.1 GI:21696785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic construct
synthetic construct
other sequences; artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gunderson, K.
Probes and decoder oligonucleotides
Patent: WO 0216649-A 365 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 bp Sequence 365 from Patent WO0216649. AX443910
                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                                                                                     AR231257
CS020856
AR404657
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AX004269
AR139887
AR139924
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AX924030
BD084559
BD084596
                                                               AR150043
BD227916
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DD210483
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GAGAGGCGTTGGTTAAGGC 22
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    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AX443910
LOCUS
DBFINITION
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AX447886
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BD141786 Novel G p
BD173668 Novel G p
BD173668 Novel G p
AR148541 Sequence
AX21529 Sequence
AX215298 Sequence
AX215298 Sequence
AX215298 Sequence
AX247840 Sequence
AX247840 Sequence
AX298773 Sequence
AX298773 Sequence
AX298773 Sequence
AX298773 Sequence
CX101953 Sequence
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AX447886 Sequence
AX538707 Sequence
AR036420 Sequence
                                                                                                       October 16, 2006, 13:57:30 ; Search time 590.797 Seconds (without alignments) 2597.742 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                  GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                        1796954
                                                                                                                                                                                                                                                                         6366136 seqs, 31973710525 residues
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                 24
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Maximum Match 100%
Listing first 45 summaries
                                                                             nucleic search, using sw model
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AX44786
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129861
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AX1529
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AX21
                                                                                                                                                                                                                             IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                               US-10-604-726A-6034
24
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9b_pat.,
9b_pl..,
9b_r..,
9b_sv..,
9b_un.,
9b_vi.,
9b_brig.,
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Match
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12.8
12.8
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Perfect score:
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Gaps

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wytheric construct
synthetic construct
synthetic construct
other sequences; artificial sequences.

1 (bases 1 to 28)
RS Terao, Y. and Shintani, Y.
ROVEL G protein coupled receptor protein and its DNA
PAREDA CHEMICAL INDUSTRIES LTD, YASUKO TERAO, YASUSHI SHINTANI
OS Artificial Sequence
NN WO 0216607-A/34
PD 28-FEB-2002
PF 23-AUG-2000 NO 2001JP0007209
PR 24-AUG-2000 JP 00P 253862
PR 24-AUG-2000 JP 00P 253862
PR 24-AUG-2000 JP 00P C121NIS/11, COTK14/47, C12NS/10, COTK14/705, G01N33/50, G01N33/15, PC C12P21/02,
PC C12P21/02,
PC C12P21/02
CC Novel G protein coupled receptor protein and its DNA FH Key
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Novel G protein coupled receptor protein and its DNA FH
Location/Qualifiers
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Novel G protein coupled receptor protein and its DNA.
BD141786
BD141786.1 GI:23236731
WO 0216607-A/34.
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                                                                                                                                                                                                                                      linear
                                                                                  2; Indels
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                                                   Length
                                                                                                                                                                                                                                                                                                                                                     Unclassified.

1 (bases 1 to 22)
Seizinger,B.R., Kley,N.A. and Bianchi,A.B.
NF2 isoforms
Patent: US 5578462-A 12 26-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.5%; Score 13.8; DB 2; Best Local Similarity 70.6%; Pred. No. 5.4e+05; Matches 12; Conservative 3; Mismatches 2;
                                             Score 13.8; DB 2;
Pred. No. 5.4e+05;
3; Mismatches 2;

    .28
    /organism="synthetic construct"
/mol_type="genomic DNA"

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/organism="unknown"
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                   22 bp
Sequence 12 from patent US 5578462.
129861
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17 AGAGGAGCTGGTTCAGG 1
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                                               y Match 57.5%;
Local Similarity 70.6%;
hes 12; Conservative
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                                                                                                                    3 AGAGGGGCUGGUUAAGG
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                                                                                                                                                                                                                                                                                                                                             Unknown
                                               Query Match
Best Local S:
Matches 12
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I29861/c
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BD141786
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Nuclear hormone receptor ligand binding domain
Patent: WO 0270557-5, 6 12-SEP-2002;
Inpharmatica Limited (GB)
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                                                                                                                    1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
                                                                                                                                                                                                                                     Query Match 65.8%; Score 15.8; DB 2; Length 25; Best Local Similarity 73.7%; Pred. No. 6.1e+04; Matches 14; Conservative 3; Mismatches 2; Indels
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Seizinger, B.R., Kley, N.A. and Bianchi, A.B.
NF2 isoforms
Patent: US 5872214-A 12 16-FEB-1999;
Location/Qualifiers
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/organism="synthetic construct"
/ordanism="synthetic bla"
/mol_type="unassigned bla"
/db_xref="taxon:32630"
/note="LBDG3 Reverse primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                            Gunderson, K.
Probes and decoder oligonucleotides
Patent: WO 0216649-A 4341 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers
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   other sequences; artificial sequences
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Sequence 12 from patent US 5872214.
AR036420
AR036420.1 GI:5953088
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synthetic construct
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Best Local Similarity
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AR036420/c
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AX538707/c
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BD173668 LOCUS

RESULT 7

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Matches

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AUTHORS TITLE

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REFERENCE

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PC A61P25/08,
PC A61P25/08,
PC A61P25/08,
PC A61P25/08,
PC C07K16/28,A61P27/16,A61P29/00,A61P31/04,A61P37/08,A61P43/00,
PC C07K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/
PC C07K16/28,C12N1/19,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/
PC G01N33/50,G01N33/50,G01N33/53,G01N33/566//A61K31/7125 PC
A61K31/713,A61K35/76,
PC A61K48/00,C12N15/00,C12N5/00
CC NOVel G procein coupled receptor protein and its DNA FH Key
Location/Qualifiers
OS Artificial Sequence
PN 07200235977-A/34
PD 26-NOV-2002
PF 23-NUOV-2001
PF 23-NUOV-2001
PF 23-NUOV-2001
PC CI2N15/09,A61R45/00,A61P1/04,A61P1/10,A61P1/12,A61P1/14,A61P1/PC
PC CI2N15/09,A61R45/00,A61P1/04,A61P1/10,A61P1/10,A61P1/10,A61P1/10,A61P1/10,A61P9/10,A61P9/10,A61P9/10,A61P9/10,A61P9/10,A61P9/10,A61P9/12,A61P1/100,A61P1/106,A61P1/3/PC
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                                                                                                                                                                                    A61P13/08, A61P15/04, A61P15/06, A61P15/08, A61P15/14, A61P25/00,
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Smith, K.E., Borden, L.A., Weinshank, R.L. and Hartig, P.R.
DNA encoding taurine and GABA transporters and uses thereof
Patent: US 6225115-A 23 01-MAY-2001;
Location/Qualifiers
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Location/Qualifiers
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Pred. No. 1e+06;

    .28
    ^organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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    .25
    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 23 from patent US 5658786.
162320
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Sequence 23 from patent US 6225115.
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Best Local Similarity 66.7
Matches 12; Conservative
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AR148541/c
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PF 02-FEB-2001 JP 01P 026798
PI TETSUTA OTAKI XASUSHI MASUDA, YOSHIHIRO TAKATSU PC
C12N15/12, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C07K14/ PC
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synthetic construct
other sequences; artificial sequences.
(Dases I to 28)
Otaki,T., Masuda,Y. and Takatsu,Y.
Novel physiologically active peptide and use thereof
Patent: WO 02062996-A 23 15-AUG-2002,
TAKEDA CHEMICAL INDUSTRIES LTD, TETSUYA OTAKI, YASUSHI MASUDA,
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BD181737
BD181737.1 GI:30792655
JP 2002335977-A/34.
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Novel physiologically active peptide and use thereof.
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other sequences.
I bases 1 to 28)
Terao, Y. and Shintani, Y.
Novel G protein coupled receptor protein and its DNA
Patent: JP 2002335977-A 34 26-NOV-2002;
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                                                           Length 28
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Pred. No. 7.9e+05;
3; Mismatches 6;
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// Organism="synthetic construct"
//mol_type="genomic DNA"
/db xref="taxon:32630"
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     /db_xref="taxon:32630"
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WO 02062996-A/23
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WO 02062996-A/23.
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l Similarity 60.9%;
14; Conservative
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 741 16-AUG-2001;
RIBOYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
patent: WO 0159103-A 742 16-AUG-2001;
RIBOZYME PHARMACEUTIALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) MCSwiggen, James (US); Chowrira, Bharat M. (US) Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/mol_type="unassigned RNA"
/nol_te="Nucleic Acid"
                                                                                                                                                                          Score 13; DB 2;
Pred. No. 1.4e+06;
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/mol type="unassigned RNA"
/db_xref="taxon:32633"
/nofe="Nucleic Acid"
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Sequence 741 from Patent WO0159103.
AX215299
AX215299.1 GI:15525342
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Sequence 742 from Patent WO0159103.
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15 TGAGAGGGCTGG 3
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AX215300/c
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Smith, K.E., Weinshank, R.L., Borden, L.A. and Hartig, P.R.
DNA encoding rat taurine transporter and uses thereof
Patent: US 568786-A 23 19-AUG-1997;
Location/Qualifiers
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Pred. No. 1e+06; 
3; Mismatches 3; Indels
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/nofe="Nucleic Acid"
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Patent: WO 0159103-A 740 16-AUG-2001;
                                                                                                                                                                                             /organism="unknown"
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AX215298
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Sequence 739 from Patent WO0159103.
AX215297
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Best Local Similarity 66.7%;
Matches 12; Conservative
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Patent: WO 0183749-A 407 08-NOV-2001,
WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center (US)
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
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1. 20
/organism="Mus sp."
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/db_xref="taxon:10095"
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Sequence 407 from Patent WO0183749.
AX298773.1 GI:17128763
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AX298773/C
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Sequence:

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Balzergue, S.

Balzergue, S.

Direct Submission

Submitted (12-0CT-2003) Balzergue S., UWRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR ware directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

Location/Qualifiers
                  A2945526 2M0206122
A294898 2M0212C15
A294899 1 2M0212C23
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A2802448 2M0061B20
CG725337 1119084H1
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CG73538 2M0251H09
A1183338 Qd41412.x
                                                                                                           AL498874 T. brucel
AZ346729 IMO082A10
AZ851549 2MO153P13
AZ786348 2MO013K14
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CZ472926 dQZ69-3p
AZ406476 IMO175B15
AZ466736 IMOZ66A16
CG777040 1119046G1
CZ473194 d03135-5p
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AA978171 ny36f08.8
AZ786207 2M0031O04
CW020366 GC0625 TI
                                                                                                                                                                                                                                                                                                                                                                          AJ591134 12-JAN-2004 27 bp DNA linear GSS 15-JAN-2004 Arabidopsis thallana T-DNA flanking sequence, left border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences
                                                                                                                                                                                                                                                                                  AZ665590 1M0547D08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                     AJ591134.1 GI:37940758
GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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EMBO Rep. 3 (12), 1152-1157 (2002)
12446565
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AZ346729
AZ851249
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CZ472926
CZ472926
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CG717040
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AZ460346
CG717040
AZ59216
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                               AZ948983
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AZ802448
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CZ443020
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AI183338
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CW020366
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 AJS91134 Arabidops
AZ806300 2M0068F13
CZ443094 IBBBD03.f
A1473941 tm04c11.x
R89803 yp91b12.r1
AG613296 Escherich
AJ531105 Arabidops
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AB081884 Drosophil
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AZ820085 2M0048M20
AZ820085 2M0048M20
AZ820085 2M009201
AJ591135 Arabidops
AZ820085 2M009201
                                                                           ; Search time 1032.18 Seconds (without alignments) 1300.222 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                            56556
                                                                                                                                                                                                      48236798 segs, 27959665780 residues
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ATH531105
AZ346559
AZ654730
AZ970595
CG712990
CG725093
AB081884
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Maximum Match 100%
Listing first 45 summaries
                                                      nucleic search, using sw model
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seq length: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ806300 24 bp DNA linear GSS 20-FEB-2001 SM068F13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0068F13 F, genomic survey sequence. AZ806300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
University of Utah Genome Center
University of Utah Genome Research Bldg., 20 S. 2030 E., SLC,
          /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
1. .27
/note="T-DNA flanking sequence
left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-"
/clone_lib="Mouse_lokb_plasmid UGCIM library"
/note="Vector: PWD42tv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, W., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                             Score 13.4; DB 14; Length 27; Pred. No. 3.1e+05;
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Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: F column: 13
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon:10090"
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/clone="580B05"
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                                                                                                                                                                                                                                              11; Conservative
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Fax: 801 585 7177
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AZ806300
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/clone_lib="HIV-vector integration sites from vell-expressed proviruses in human Jurkat T cells" /note="Vector: LTR-Tat-IRES-GFP (pEV71); we have investigated regulatory sequences in noncoding human blat are associated with repression of an integrated human inmunodeficiency virus type I (HIV-1) promoter: HIV-1 integration results in the formation of precise and homogeneous junctions between viral and host DNA, but integration takes place at many locations. Thus, the variation in HIV-1 gene expression at different integration sites reports the activity of regulatory sequences at nearby chromosomal positions. Wegative regulation of HIV transcription is of particular interest because of its association with maintaining HIV in a latent state in cells from infected patients. To identify chromosomal regulators of HIV transcription, we infected Jurkat T cells with an HIV-based vector transducing green fluorescent protein (GFP) and separated cells into
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (Dases 1 to 28)
Lewinski, M.K., Bisgrove, D., Shinn, P., Chen, H., Hoffmann, C., Hannenhalli, S., Verdin, E., Berry, C.C., Ecker, J.R. and Bushman, F.D. Genome-wide analysis of chromosomal features repressing human immunodeficiency virus transcription

J. Virol. 79 (11), 6610-6619 (2005)
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                       52.5%; Score 12.6; DB 11; Length 24; llarity 57.9%; Pred, No. 6.9e+05; Conservative 4; Mismatches 4; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bushman@mail.med.upenn.edu
Class: PCR with specific primers.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:9606"
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CZ443094.1 GI:62379366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 215 573 8732
Fax: 215 573 4856
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yp91b12.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194783 5' similar to gb:X63526 ELONGATION FACTOR 1-GAMMA HOMO SAPIENS SOURCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Werck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: estewateon.wustl.edu
Insert Size: 1193
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; race considered overall poor quality
Insert Length: 1193 Std Error: 0.00
Seq primer: MI3RPI
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The fosses 1 to 25)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Pred. No. 1.3e+06;
3; Mismatches 0;
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/mol_type="mRNA"
/db_xref="GDB:3763833"
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/clone="IMAGE:194783"
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                                    GAGAGGGCUGGUUAAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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12 GGGCTGGTTAA
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Best Local Similarity
Matches 9; Conserva
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JOURNAL
COMMENT
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R89803/c
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populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profiling, Low-level GFP expression correlated with integration in (i) gene
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1473941 22 bp mRNA linear EST 09-MAR-1999 tm04c11.x1 NCI CGAP Co14 Homo sapiens cDNA clone IMAGE:2155604 3' similar to TR:\(\overline{0}\)06459 \(\overline{0}\)06459 \(\overli
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
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Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (1997)
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Gaps

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Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (8) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/clone="225H06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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1 (Dases II. 1. 22)
1 (Dases II. 1. 22)
1 (Dases II. 2. 22)
1 (Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R. Understand inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                       1. .28
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ecotype="Wassilewskija"
1. .28
/note="T-DNA flanking sequence
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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Location/Qualifiers
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AZ346559.1 GI:10425796
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                                                                                                           GSS 24-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-778-2004) Takashi Horiuchi, National Institute for Basic Biology, Gene Expression and Regulation II; 38 Nishigo-naka, Myodaijitor, Okazaki, Aichi 444-8585, Japan (E-mail:kishori@mibb.sc.jp, Tel:81-564-55-7690, Fax:81-564-55-7695) Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                 Hayashi,K., Morooka,N., Mori,H. and Horiuchi,T.
A more accurate sequence comparison between genomes of Escherichia
coli K12 W3110 and MG1655 strains
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T-DNA integration into the Arabidopsis genome depends on sequences
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                                                                                                                                                                                                                                               Bscherichia coli K12
Bscherichia coli K12
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
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                                                                                                   AG613296 27 bp DNA linear GSS 24-J.
Escherichia coli K12 MG1655 DNA, clone: 431F, genomic survey
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This is located within REP element."
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AJ531105.
AJ531105.1 GI:26799365
GSS, left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/strain="K12"
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Hayashi, K., Morooka, N. and Horiuchi, T.
Direct Submission
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/db_xref="taxon:83333"
/clone="431F"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gillygl)AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-GG1d (Stratagene) cells and selected for ampicillin resistance."
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 21)
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/note="Wector: PWD4Zuv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
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Insert Length: 10000 Std Brror: 0.00
Plate: 0529 row: P column: 05
Seg primer: CGTTGTAAAACGACGGCCAGT
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/db_xref="taxon:10090"
/clone="UUGC1M0081M15"
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                                                          /sex="Male
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Fax: 801 585 7177
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/gas="model" coll strain XL10-Gold, T1-resistant, F-"
/slab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone 11br=whouse 10kb plasmid UUGCIM library.
/clone 11br=whouse 10kb plasmid UUGCIM library.
/note="Wector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil 4772114 [gb] AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (sraatagene) cells
and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognath; Murcidea; Muridae; Mus.

1 (bases 1 to 27)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
L Unpublished (200)
Contact: Robert B. Weiss
University of Utah Genome Center
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2M0243I18R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243I18 R, genomic survey sequence.
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Fax: 801 585 7177
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/ULGITIBLE TERM HEAD TO THE TABLE TO THE TRANSMERS TO THE TABLE TERM HEAD THE TABLE TERM HEAD THE TE
/dec_Badge="DH10B"
/lab host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/clone_lib="1119 - RescueMu Grid AA"
/clone_lorgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site l: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu,' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG725093 20-OCT-2003
1119083H11.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
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Unpublished (2001)
Contact: Walbot V
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 27)
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Reverse complemented post-ligation sequence from source sequence.
Plate: 1119083 row: H column: 11
Class: transposon-tagged.
Location/Qualifiers
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Stanford University
855 California Ave, Palo Alto, CA 94304,
11 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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/organism="Zea mays"
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Local Similarity 61.1%;
les 11; Conservative
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                                                                                                                                                                                                /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: FWD42nv; Purlfied genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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1 (Sea to 27)
Walbot, V.
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855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221
Email: walbot@stanford.edu
Email: walbot@stanford.edu
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119029 row: H column: 12
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/cultivax="mixed background W23/A188/B73/K55"
/db xref="taxon:4577"
/tisue_type="leaf"
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48.3%; Score 11.6; DB 11; Length 27;
Best Local Similarity 61.1%; Pred. No. 1.9e+06;
Matches 11; Conservative 3; Mismatches 4; Indels (
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                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                              'db xref="taxon:10090"
                                                                                                                                /clone="UUGC2M0243I18"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleoride kinase. Adaptor oligonucleorides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWAP2 (gal 4732114[gbl]AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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A2375590.
A2375590.1 GI:10489290
GSS.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/63 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
Islam, H., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokee, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact PAL.
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                                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: M column: 20
Seg primer: CGTYGTAAACGACGACCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 25.
Location/Qualifiers
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Mus musculus
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AB081884 30 bp DNA linear GSS 25-FEB-2003
Drosophila melanogaster DNA, clone:1(2)SH2 0127, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-MAR-2002) Suwan Oh, The Laboratory of Immunobiology, National Institutes of Health, National Cancer Institute, Frederick; 1050 Boyles st., Frederick, Maryland 21702-1201, USA (E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Mus.
1 (bases 1 to 25)
                                         BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oh,S.W., Kingsley,T., Shin,H.H., Zheng,Z., Chen,H.W., Chen,X., Wang,H., Ruan,P., Moody,M. and Hou,S.X.
A p-element inscrtion screen identified mutations in 455 novel essential genes in Drosophila Genetics 163 (1), 195-201 (2003)
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S. Direct Submission
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                                                                                                                                                                      48.3%; Score 11.6; DB 12; Length 27; 61.1%; Pred. No. 1.9e+06;
                                                                                                                                                                                                                       4; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="1(2)SH2 0127"
                                                                                                                                                                                                                       3; Mismatches
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AUTHORS
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TITLE
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Gaps

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GSS 02-OCT-2000

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AUTHORS Dunn, D. Acyagi, A. Barber, M., Beacorn, T., Duval, B., Hamil, C., Raim, M., Mosmon, B., Pedersen, T., Raim, M., Rongerre, S., Mammould, M., Meaner, B., Pedersen, T., Raim, M., Rongerre, S., Mammould, M., Meaner, B., Pedersen, T., Raim, M., Ronger, R., Goos, R., Stokes, R., Tingey, A., von Midderhausern, A. and Wright, D., Meise, R. Tingey, A., von Midderhausern, A. and Wright, D., Meise, R. Tingey, A., von Midderhausern, A. and Wright, D., Meise, R. Tingey, A., von Midderhausern, C., Meise, R. Meise, R. Tingey, A., von Midderhausern, C., Meise, R. Meise, R. Stoke, R. Meise, R. Mei
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Query Match
47.5%; Score 11.4; DB 11; Length 30;
Best Local Similarity 52.4%; Pred. No. 2.4e+06;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps
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Qy 1 UGAGAGGGCUGGUJAAGGG 21

Db 27 TGAAAAGGAGTTGTTAAGGGG 7

Search completed: October 16, 2006, 15:51:23 Job time : 1034.18 secs

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Sequence 15707, A Sequence 12, Appl Sequence 13, Appl Sequence 23, Appl Sequence 27, Appl Sequence 12, Appl Sequence 119, App Sequence 51, Appl Sequence 51, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Appl
Sequence 15707, A
                                                                                                                October 16, 2006, 14:11:03; Search time 55.5789 Seconds (without alignments) 807.979 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-136-136-15707

US-08-139-12

US-08-628-145-12

US-08-295-814-23

US-09-598-9820-7

US-09-598-9820-7

US-09-578-123

US-09-578-123

US-09-578-119

US-09-166-119

US-09-119-119

US-08-119-119

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Maximum Match 100%
Listing first 45 summaries
                                                                             nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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24
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Sequence 102, App Sequence 65, Appl Sequence 102, App Sequence 102, App Sequence 102, App Sequence 102, App Sequence 65, Appl Sequence 65, Appl Sequence 65, Appl Sequence 65, Appl Sequence 11, Appl Sequence 7888, A Sequence 7888, A Sequence 7888, A Sequence 11, Appl Sequence 122139, Sequence 122139, Sequence 122139, Sequence 122139, Sequence 4100, Sequence 6122, Appl Sequence 61240, Appl Seque		G OF SOILING C 15783th America, Inc.
3 US-08-471-971-102 3 US-09-402-776-65 3 US-09-202-776-65 3 US-09-291-129-10 3 US-08-470-246-102 3 US-08-470-246-102 3 US-08-316-765-102 3 US-08-316-765-102 3 US-09-724-475-102 7 PCT-US93-08849A-65 7 PCT-US93-08849-65 7 PCT-US93-08849-65 7 US-09-396-196G-78489 3 US-09-396-196G-7889 3 US-09-396-196G-122139	ALIGNMENTS	ppplication US/08814052 5783 484710M: von der Osten, Claus Cherry, Joel R. Bjornvad, Mads E. Vind, Jesper Rasmussen, Michael Dolberg VENTION: VENTION: NEW YORK US. M. 10.5. A. 10.5. A
2.6 52.5 30 2.6 522.5 30 2.6 522.5 30 2.6 522.5 30 2.6 522.5 30 2.6 522.5 30 2.7 6 522.5 30 2.8 6 522.5 30 2.9 7 8 11.7 2 2 4 2.1 7 7 2 2 5 2.2 5 5 0 8 8 20 2.2 5 5 0 8 20		SULT 1 -08-814-052-53/C Sequence 53, Application US/08814052 Sequence 53, Application US/08814052 Sequence 53, Application US/08814052 Sequence 53, Application US/08814052 SAPPLICANT: Von der Osten, Claus APPLICANT: Cherry, Joel R. APPLICANT: Cherry, Joel R. APPLICANT: Rasmasen, Michael Dolberg TITLE OF INVENTION: OR STAINS FROM CELLI NUMBER OF SEQUENCES: 55 CORPUTES: No. 60157830 No. 6015783dis STREET: 405 Lexington Avenue, Suite 6 CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATIOS SYSTEM: DOS SOFTWARE: FRAISCO FOR Windows Version CURRENT APPLICATION DATA: 4684.204-US FILING DATE: 06-MAR-1997 CLASSIFICATION: 510 ATTORNEY AGENT INFORMATION: NAME: Lambiris, Elias J REGISTRATION FOR EQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 28 base pairs TYPE: mucleic acid STRANDEDNESS: single TOPOLOGY: linear
000 000000000 0000 0000 0000 0000 0000 0000		RESULT 1 US-08-814-052-53 Sequence 53 A SPLICANT: APPLICANT: APPLICATION TO DA APPLICANT: APPL

DB 3; Length 28;

63.3%; Score 15.2;

Query Match

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Gaps
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Pred. No. 2.5e+03;
3; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Elappy disk
COMPUTER: Elappy disk
COMPUTER: Elappy disk
COMPUTER: Elap Compatible
COMPUTER: DEM PC. COMPUTER:
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,145
FILING DATE: 04-APR-1996
CLASSIFICATION TS0
PRIOR APPLICATION NUMBER: US 08/179,738
FILING DATE: 10-JAN-1994
ATTOMENYAGENT INFORMATION:
ANAMERIA AGENT INFORMATION:
ANAMERIA AGENT INFORMATION:
ANAMERIA DELACTION DATE: 10-JAN-1994
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| Sequence 12, Application US/08628145
| Sequence 12, Application US/08628145
| Patent No. 5872214
| GENERAL INFORMATION:
| APPLICANT: Seizinger, Bernd R. APPLICANT: Riey, Nikolai A. APPLICANT: Bianchi, Albert B. TITLE OF INVENTION: No. 587214el NF2 Isoforms | VUMBER OF SEQUENCES: 26 | CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CONTRY: California | COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Robins, Roberta L.
REGIETRATION UNUBER: 33,208
REFERENCE/DOCKET INUBER: 5998-0017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 22 base pairs
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                    3 AGAGGGCUGGUUAAGG 19
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70.6%;
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Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                           Best Local Similarity 70.6
Matches 12; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
                                                                                                     single
                                                                                           STRANDEDNESS: Sing
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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     Pred. No. 5.5e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: TEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,738
FILING DATE: 10-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08179738
Sequence 12, Application US/08179738
Sequence 12, Application US/08179738
Sequence 12, Application US/08179738
Sequence 12, Application Setzinger, Bernd R.
APPLICANT: Setzinger, Bernd R.
APPLICANT: Bianchi, Albert B.
TITLE OF INVENTION: No. 5578462el NF2 Isoforms
TUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Reed & Robins
STREET: 635 BYPANT Street
CITY: Palo Alto
STRATE: California
                                                                                                                                                                                                                                      Sequence 15707, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REPRENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 80/100,678
SPRIOR APPLICATION NUMBER: 60/100,678
SPRIOR PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SSETWARE: FREESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 15707
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NAME: ROblans, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFPR: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 UGAGAGGGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 TGAGATGAGCTGCTTAACGAGT 1
                                                                              2 GAGAGGGCUGGUUAAGGCG 21
                                                                                                          20 GCGAGTGGCTGGTCAAGGCG 1
       75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 54.5
Matches 12; Conservative
     Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-15707
                                                                                                                                                                                                  RESULT 2
US-09-396-196G-15707/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-179-738-12/c
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                              Matches
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Gaps

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GENERAL INFORMATION:
APPLICANT: Miles, Andrew
APPLICANT: Males, Andrew
APPLICANT: Males, Andrew
APPLICANT: Males, Andrew
APPLICANT: Haak-Freehow, Mary
TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TRYPTASES, ACTIVE SITE MUTANTS THEREOF,
TITLE OF INVENTION: AND METHODS OF MAKING SAME
TITLE REPERENCE: 34506.104
CURRENT APPLICATION NUMBER: US/09/598,982C
CURRENT FILING DATE: 2000-06-21
PRIOR PILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 52
SOFTWARR: PARENTIN Version 3.3
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08460751
; Sequence 27, Application US/08460751
; Patent No. 5891628
; GENERAL INFORMATION:
APPLICANT: Receders, Stephen
APPLICANT: Glucksmann, Sandra
TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CONRESPONDENCE Edmonds
STREET: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PARENTIN RELEGEBER #1.0, Version #1.30
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  Length 25;
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                                          Indels
Score 13.2; DB 3;
Pred. No. 4.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Mutagenesis oligonucleotide
US-09-598-982C-7
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/413,580
FILING DATE: 03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,751
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                          Sequence 7, Application US/09598982C
Patent No. 6998260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GAGGGCUGGUUAAGGCGUCC 24
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                                                                                         5 AGGGCUGGUUAAGGCGU 22
                                                                                                                                   23 AGGTGCTGGTGAAGGCAT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                          US-09-598-982C-7
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US-08-460-751-27
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                     Best Loca
Matches
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Factor No. 6225115
GENERAL INFORMATION:
FAPLIACANT: Smitch, Kelli E. et al
TITLE OF INVENTION: DNA Encoding Taurine and GABA Transporters and Uses
TITLE OF INVENTION: Thereof
FILE REPRENCE: 40589-D
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0 - beta
LENGTH: 25
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.0%; Score 13.2; DB 2; Length 25; 66.7%; Pred. No. 4.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3, Indels
           Sequence 23, Application US/08295814E
Patent No. 5658786
GENERAL INFORMATION:
APPLICANT: Smith, Kelli E.
APPLICANT: Borden, Laurence A.
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING TAURINE AND GABA;
TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40558-B-PCT-US
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,814E
FILING DATE: DECEMBER 19, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                  E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4055:
TELECPHONE: 212-278-0400
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AGGGCUGGUUAAGGCGU 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AGGTGCTGGTGAAGGCAT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                            STREET: 1185 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
US-08-295-814E-23/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-343-361-23/c
                                                                                                                                                                                                                                                                    ADDRESSEE:
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TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY FILE REFERENCE: JHU1630-1
CURRENT APPLICATION NUMBER: US/10/059,579A
CURRENT FILING DATE: 2001-01-28
PRIOR APPLICATION NUMBER: US 09/771,357
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin version 3.1
SEQ ID NO 123
LENGTH: 19
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Sequence 119, Application US/09166186A

Patent No. 6080580

GENERAL INFORMATION:
APPLICANT: Bather, Brenda
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
APPLICANTON: Shanahan, William R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
TITLE OF INVENTION: STRESSION
FILE REFERENCE: ISPH-0356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 52.5%; Score 12.6; DB 3; Length 19; Best Local Similarity 57.9%; Pred. No. 9.1e+03; Matches 11; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.5%; Score 12.6; DB 3; Length 20; 63.2%; Pred. No. 9.1e+03; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/313,932A CURRENT FILING DATE: 1999-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: PCR antisense primer US-10-059-579A-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: antisense sequence US-09-166-186-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 119, Application US/09313932A
Patent No. 6228642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GAGGGCUGGUUAAGGCGU 22
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-313-932-119/c
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US-09-166-186-119/c
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US-10-059-579A-123/c
is equence 123, Application US/10059579A
is patent No. 6835541
is GENERAL INFORMATION:
is APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
is APPLICANT: SUKNOMAR, Saraswati
is APPLICANT: EVRON, Ella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31, Application US/09641259B
; Batent No. 6468756
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A
; APPLICANT: Bonini, James A
; APPLICANT: Borowsky, Beth E
; APPLICANT: Adham, Nika
a APPLICANT: Thompson, Thelma O.
; TITLE OF INVENTION: DNA Encoding SNORF25 Receptor
; FILE REFRENCE: 1795/56095-B/JPW/ADM
; CURRENT APPLICATION UNMBER: US/09/641,259B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/4413
; PRIOR FILING DATE: 1299-02-22
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PALENTIN VUMBER: US 09/355,376
; SOFTWARE: PALENTIN VUMBER: US 09/355,376
; SOFTWARE: PALENTIN VUMBER: US 09/355,376
; SOFTWARE: PALENTIN VERSION 3.1
; SEQ ID NO 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.3%; Score 12.8; DB 2; Best Local Similarity 62.5%; Pred. No. 7.3e+03; Matches 10; Conservative 4; Mismatches 2;
                          NAME: Coruzzi, Laura A.
REGISTATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7638-005
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Primer/ Probe US-09-641-2598-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 GCUGGUUAAGGCGUCC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||: ::||||||||
| GCTCTTTAAGGCGTCC 16
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ORGANISM: Artificial Sequence
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-460-751-27
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US-09-641-259B-31/c
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GENERAL INFORMATION:
APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH
APPLICANT: COGANISATION
TITLE OF INVENTION: Polyphenol oxidase genes from banana, lettuce, tobacco and
TITLE OF INVENTION: pineapple
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC; OTHER INFORMATION: PRIMER; OTHER INFORMATION: PRIMER 1
19.09-520-373D-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
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Pred. No. 9.2e+03;
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Pred. No. 9.5e+03;
               CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/37,710
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR PILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-06-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/443,067
CURRENT FILING DATE: 1999-11-18
EARLIER APPLICATION NUMBER: US 08/976, 222
EARLIER APPLICATION NUMBER: PCT/AU98/00362
EARLIER APPLICATION NUMBER: PCT/AU98/00362
EARLIER APPLICATION NUMBER: PCT/AU98/00362
EARLIER FILING DATE: 1998-05-19
EARLIER FILING DATE: 1997-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 52.5%; Score 12.6; D
1 Similarity 63.2%; Pred. No. 9.2e
12; Conservative 3; Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 63.2%;
Matches 12; Conservative
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SEQ ID NO 45
LENGTH: 25
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Best Local Similarity
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APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: RAW, Hee Kyung
TITLE OF INVENTION: Oligonuclectide for detection and identification of Mycobacteria
FILE REFERENCE: PPO5020/PCT
CURRENT PELLON NUMBER: US/99/980,052
CURRENT FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: KR 10-1999-0019633
PRIOR FILING DATE: 1999-05-29
PRIOR PELLING DATE: 1999-05-29
PRIOR PILING DATE: 1999-06-29
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TITLE OF INVENTION: RETINAL PIGMENTED EPITHELLUM DERIVED NEUROTROPIC FACTOR
                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 9.1e+03;
3; Mismatches 4; Indels
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Pred. No. 9.1e+03;
3; Mismatches 4;
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10S-08-520-313D-31/c
; Sequence 31, Application US/08520373D
; Patent No. 6451763
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Patent No. 6670130
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Chader, Gerald J
Becerra, Sofia P
Johnson, Lincoln V
                                                                                                                                                                                                                        52.5%;
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63.2%;
                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Tombran-Tink, Joyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                              ; OTHER INFORMATION: Synthetic US-09-313-932-119
                                                                                                                                                                                                                                               Best Local Similarity 63.2
Matches 12, Conservative
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Best Local Similarity 63.2
Matches 12; Conservative
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SOFTWARE: Kopatentin 1.71
SEQ ID NO 51
LENGTH: 20
NUMBER OF SEQ ID NOS: 501
SEQ ID NO 119
LENGTH: 20
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APPLICANT:
APPLICANT:
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APPLICANT:
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Search completed: October 16, 2006, 14:47:12 Job time : 56.5789 secs

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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US108_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
17: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
18: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
18: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Sequence 1286104,
Sequence 1056699,
Sequence 594065,
Sequence 1286102,
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Sequence 310484,
Sequence 310485,
Sequence 310486,
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Sequence 4341, Ap
Sequence 751276,
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Sequence 62329, A
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872.534 Million cell updates/sec
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                                                                                                                                                  October 16, 2006, 14:16:09; Search time 337.985 Seconds
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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-036-317-751276

3 US-11-036-317-75884

1 US-11-036-317-648052

1 US-10-310-914A-310484

US-10-310-914A-310486

US-10-310-914A-310487

US-10-310-914A-310487

US-10-310-914A-594059

US-10-310-914A-1286104

US-10-310-914A-1286104

US-10-310-914A-1286104

US-10-310-914A-1286102
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Listing first 45 summaries
                                                                                                  OM nucleic - nucleic search, using sw model
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24
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Match Length DB
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65.0
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63.3
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Perfect score:
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Sequence 463132, Sequence 470368, Sequence 473457, Sequence 537085,	Sequence 657262, Sequence 713203, Sequence 798014, Sequence 752575, Sequence 77570,	2 44	Sequence 888594, Sequence 892234, Sequence 966783, Sequence 1006049, Sequence 1006049,	Sequence 7, Appli Sequence 1339473, Sequence 605791, Sequence 213436, Sequence 884459,
US-11-121-849-463132 US-10-719-900-470368 US-10-719-900-473457 US-11-036-317-537085	SU SU SU	US-10-310-914A-707100 US-10-310-914A-1006052 US-10-469-866-23 US-10-310-914A-24322 US-10-719-956-115625 US-10-719-956-115625	US-10-719-900-888594 US-11-036-317-892224 US-11-036-317-966783 US-11-121-849-363 US-10-310-914A-1006049 US-10-330-914A-224323	US-10-504-589A-7 US-10-310-914A-1339473 US-10-719-956-605791 US-11-036-317-213436 US-11-036-317-884459
9 9 5	5555	11161188	111111111111111111111111111111111111111	11 11 13 13
25 25 25 25 25	22122	2 2 2 2 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5	25 25 25 26 27	21 25 25 25 25 25
15.2 63.3 15 62.5 15 62.5 15 62.5	55 62. 55 62. 88 61.	مەمەمەمە	ب به به به به	14.4 60.0 14.4 60.0 14.4 60.0 14.4 60.0 14.4 60.0
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ALIGNMENTS

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RESULT 1

URSJULT 1

URSDULT 2

URSDULT 1

URSDULT 2

URSDULT 2

URSDULT 2

URSDULT 3

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ORGANISM: Artificial Sequence
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US-11-036-317-751276/c
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                                                                                                                                                                                                                                                                67.5%; Score 16.2; DB 9; Length 25; 66.7%; Pred. No. 1.4e+03;
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; Sequence 4341, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; FILE REFERENCE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SEQ ID NOS: 4768
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 888593
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 365, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
    APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
FILE REPERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR PILING DATE: 2000-08-25
; PRIOR PILING DATE: 2000-08-25
; PRIOR PILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; ROWDER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 365
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US-09-940-185-365
                                                                                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                23 GAAGGGCTAGTTAAGGCTTCC 3
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Matches 14; Conservative
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US-10-719-900-888593
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US-09-940-185-365
                                                                                                                                                                  TYPE: DNA
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Sequence 751276, Application US/11036317

Sequence 751276, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williams, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REPERENCE: 3654, Ala

FILE PEPRICANT: WILLIAG DATE: 2005-01-13

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Sequence 508584, Application US/11036317
Publication No. US20000214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analygis of Alternative Splicing in Mouse
TITLE OF INVENTION: Method of Analygis of Alternative Splicing in Mouse
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
FRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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                                                                       Length 25;
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; OTHER INFORMATION: Computer Generated Probe Sequence. US-09-940-185-4341
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Pred. No. 2.1e+03;
4; Mismatches 2;
                                                                    Query Match 65.8%; Score 15.8; DB 3; Best Local Similarity 73.7%; Pred. No. 2.1e+03; Matches 14; Conservative 3; Mismatches 2;
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25 AGAGGCCCTGGTTCAGGAGTCC 4
                                                                                                                                                                          2 GAGAGGGCUGGUUAAGGC 20
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25 TCAAAGGGGCTGGTTAAGG 7
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68.4%;
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Best Local Similarity 68.41
Matches 13; Conservative
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; ORGANISM: Mus musculus
US-11-036-317-751276
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CORGANISM: Mus musculus
US-11-036-317-508584
                                                                         Query Match
Best Local Similarity
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APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: uses thereof
CURRENT APPLICATION NUMBER: US/10/310, 914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 310486
LENGTH: 21
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Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Biller, Kvuzat
APPLICANT: Biller, Kvuz
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                                                                                                                                                                                                                  Score 15.2; DB 11;
Pred. No. 4.1e+03;
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Pred. No. 4.1e+03;
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75.0%; Pred. No. 4.1e+03;
tive 2; Mismatches 3;
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75.0%; Pred. No. 4...
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; Sequence 310486, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              1 UGAGAGGGCUGGUUAAGGC 20
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 310485
LENGTH: 21
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Best Local Similarity 75.0
Matches 15; Conservative
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Best Local Similarity 75.0
Matches 15; Conservative
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                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                          ; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-310485
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ORGANISM: Human
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US-10-310-914A-310484/C

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S-10-310-914A-310484/C

S-10-310-914A-310484/C

S-10-310-914A-310484/C

S-10-310-914A-310484/C

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwarch, Reacc

APPLICANT: Bentwarch, Reacc

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARKE: PatentIn version 3.3

SEQ ID NO 310484

LENGTH: 21
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US-10-914A-310485/c
US-10-310-944A-310485/c
Sequence 310485, Application US/10310914A
Sequence 310485, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kuvzat
APPLICANT: Shiler, Kuvzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: USOS 1200.5010
CURRENT APPLICATION UNMERE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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                                                                          Sequence 648052, Application US/11036317
Sublication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Milliams, Alan
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Best Local Similarity 63.6%; Pred. No. 2.0
Matches 14; Conservative 4; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Mus musculus US-11-036-317-648052
                                                                       US-11-036-317-648052/c
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Search completed: October 16, 2006, 16:22:41 Job time : 338.985 secs
; SEQ ID NO 1056699
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1056699
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ORGANISM: Human
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US-10-310-914A-1286104/c
; Sequence 1286104, Application US/10310914A
; Publication No. US2060003322A1
; Publication No. US2060003322A1
; GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: Uses thereof
; TITLE OF INVENTION: Uses thereof
; TITLE OF INVENTION: Uses thereof
; CURRENT PLILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1286104
. LENGTH: 21
                                                                                                                                 APPLICANT: Bentwitch, Isaac
APPLICANT: Bentwitch, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bloinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERRNCE: 06087.0200. CPUSO1
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 594029
LENGTH: 21
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US-10-914A-1056699/C
US-10-914A-1056699/C
US-10-914A-1056699 Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Esaac

TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06609.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILIC DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3
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                                                                     ; Sequence 594029, Application US/10310914A; Publication No. US20060003322A1; GENERAL INFORMATION:
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Sequence 594065, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich. Isaac

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION:

FILE REPERENCE: 06097.0200.CPUS01

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

CURRENT APPLICATION NUMBER: US/10/310, 914A

CURRENT PLING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 594065

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63.3%; Score 15.2; DB 11;
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iive 1; Mismatches 3;
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Best Local Similarity 85.0
Matches 17; Conservative
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| EMC Celerra SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| EMC Celerra SIDS3/ptodata/2/pubpna/US07 NEW PUB.seq:*
| EMC Celerra SIDS3/ptodata/2/pubpna/US08 NEW PUB.seq:*
| EMC Celerra SIDS3/ptodata/2/pubpna/PCT NEW PUB.seq:*
| EMC Celerra SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq:*
| EMC Celerra SIDS3/ptodata/2/pubpna/US10 NEW PUB.seq:*
| EMC Celerra SIDS3/ptodata/2/pubpna/US11 NEW PUB.seq:*
| EMC Celerra SIDS3/ptodata/2/pubpna/US1 NEW PUB.seq:*
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88277, A
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32918, A
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32920, A
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113852,
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Sequence 25472, A
Sequence 101402,
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Sequence 792144,
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US-11-348-413-797012

US-11-217-529-41374

US-11-217-529-41374

US-11-217-529-41374

US-11-217-529-11977

US-11-317-529-11977

US-11-348-413-32918

US-11-348-413-32921

US-11-348-413-620816

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Publication No. US20060099612A1

GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAWURA, VOSHHIRO

APPLICANT: NAKAWURA, VOSHHIRO

APPLICANT: NORMAN, YUKIKO

APPLICANT: FUJIWIRA, TOMOKO

APPLICANT: FUJIWIRA, TOMOKO

APPLICANT: FUJIWIRA, TOMOKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 5-38-285

CURRENT FILING DATE: 2005-09-02

FRIOR APPLICATION NUMBER: US 10/932,182

PRIOR APPLICATION NUMBER: US 10/932,182
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Publication No. US20060099612A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAWURA, NORIHISA
APPLICANT: FUJIWIRA, TOWOKO
APPLICANT: FUJIWIRA, TOWOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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US-11-217-529-1282

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US-11-217-529-125663

US-11-217-529-135070

US-11-217-529-136635

US-11-217-529-136635

US-11-217-529-136635

US-11-348-413-130142

US-11-348-413-152231

US-11-348-413-355681

US-11-348-413-365682

US-11-348-413-365682

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Query Match
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CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
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Pred. No. 6.3e+03;
4; Mismatches 6; Indels
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Pred. No. 6.3e+03;
4; Mismatches 1;
; FILE REFERENCE: S-38-285; CURRENT APPLICATION NUMBER: US/11/217,529; CURRENT FILING DATE: 2005-09-02; PRIOR APPLICATION NUMBER: US 10/932,182; PRIOR FILING DATE: 2004-09-02; NUMBER OF SEQ ID NOS: 197023; SOFTWARE: PatentIn version 3.3; SOFTWARE: PatentIn version 3.3; SELENGTH: 25
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US-11-217-529-36679/c
US-11-217-529-36679, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMIRA, NORIHISA
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
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Best Local Similarity 66.7
Matches 10; Conservative
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Best Local Similarity
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US-11-217-529-101402/c
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APPLICANT: Mounts, william M
APPLICANT: Mounty, Blien
APPLICANT: Murphy, Blien
APPLICANT: Olmsted, Stephen
CURRENT BILING DATE: 2006-084100
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/USOS/035471
PRIOR APPLICANTON NUMBER: US 11/243,445
PRIOR PRILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
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APPLICANT: Mounte, William M
APPLICANT: Murphy, Ellen
APPLICANT: Mounte, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
FURRENT APPLICATION NUMBER: US/11/348,413
FURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/USO5/035471
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NAME/KEY: misc_feature
LOCATION: (1): (125)
OTHER INFORMATION: SEQ ID NO: 5316; WANGIUNLH_at; Start 930; Stop 954;
OTHER INFORMATION: 000010000000000
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                                                                                                                                                                                                                                              55.0%; Score 13.2; DB 8; Length 25; 66.7%; Pred. No. 7.8e+03;
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                                                                                                                                                                                                                                                                                                                3, Mismatches
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; GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 792144, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                            ; TYPE: DNA; CRCharomyces pastorianus US-11-217-529-36679
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NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 8679
LENGTH: 25
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Matches 12; Conservative
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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US-11-348-413-877012/c
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US-11-348-413-792144
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APPLICANT: NUKACN YOSHITED
APPLICANT: NAKACN, YOSHITEN
APPLICANT: NAKACNICA, YOSHITEN
APPLICANT: NAKACNICA, YOSHITEN
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJINAN, TOWOKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 8-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT APPLICATION NUMBER: US 10/932,182
PRIOR RILING DATE: 2004-02
PRIOR FILING DATE: 2004-02
NUMBER OF SEQ ID NOS: 197023
SOCTWARE: Patentin version 3.3
SOCTWARE: Patentin version 3.3
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Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: FUJIMURA, YORKIN
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKAI, YOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 5-38-285
               METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                         Length 25;
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1 Similarity 57.1%; Pred. No. 9.6e+03;
12; Conservative 4; Mismatches
                                                       CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 41374
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
                                                                                                                                                                                                                                                                               ) ORGANISM: Saccharomyces pastorianus
US-11-217-529-41374
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-88277
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Best Local Similarity
Matches 12; Conserv
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Matches 12; Conserv
               TITLE OF INVENTION:
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NAME/KEY: misc_feature
LOCATION: (1)..(25)
OTHER INFORMATION: SEQ ID NO: 7631; WANOIUMIA_at; Start 143; Stop 167;
OTHER INFORMATION: 000000011100000
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Publication No. US20060099612A1
GENERAL INCOMATION:
GENERAL INCOMATION:
GENERAL INCOMATION:
APPLICANT: SUNYORY LIMITED
APPLICANT: NAKAWURA, NORHIISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOWKOO
APPLICANT: FUJIMURA, TOKHHIIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILLE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
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PRIOR FILING DATE: ZUUS-L. TO PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: Z005-10-05
PRIOR PELIORION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 877012
LENGTH: 25
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PRIOR FILING DATE: 2004-09-02
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Publication No. US20060099612A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Saccharomyces pastorianus US-11-217-529-29983
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
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SOFTWARE: Patentin version 3.3
SEQ ID NO 29983
LENGTH: 25
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Gaps

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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-177967
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OTHER INFORMATION: probe
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; Sequence 177967, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:
   APPLICANT: NAKAO, YOSHHIRO
; APPLICANT: NAKAONA, VORIHIRA
; APPLICANT: RODAMA, VUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHHHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT PILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
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                                                                                                                                                          Query Match 53.3%; Score 12.8; DB 8; Length 25; Best Local Similarity 75.0%; Pred. No. 1.2e+04; Matches 12; Conservative 2; Mismatches 2; Indels
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                                                                                        TYPE: DNA ORGANISM: Saccharomyces pastorianus
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4581
LENGTH: 25
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SOFWARE: Patentin version 3.3
SEQ ID NO 177967
LENGTH: 25
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US-11-217-529-177967/c
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Murphy, Ellen
APPLICANT: Olimated, Stephen
TITLE OP INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REPERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT PILING DATE: 2006-02-07
PRIOR APPLICANTON NUMBER: US 11/243,445
PRIOR PILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2004-10-05
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 32918
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APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT APPLICATION NUMBER: PCT/USO5/035471
PRIOR FILING DATE: 2006-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR PLICATION NUMBER: US 60/615,573
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) LOCATION: (1)..(25)

) OTHER INFORMATION: SEQ ID NO: 423; WANOIUJBU; Start 271; Stop 295;

) OTHER INFORMATION: 1111111100000000

US-11-348-413-32918
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Query Match 53.3%; Score 12.8; DB 8; Length 25; Best Local Similarity 62.5%; Pred. No. 1.2e+04; Matches 10; Conservative 4; Mismatches 2; Indels
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; Sequence 32918, Application US/11348413
; Publication No. US20060160121A1
; GRNEAL INFORMATION:
APPLICANT: Wyeth
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Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Best Local Similarity 62.5
Matches 10; Conservative
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us-10-604-726a-6034.szlm30.rnpbn

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RESULT 15
US-11-348-413-32920
15 Sequence 32920, Application US/11348413
15 Publication No. US20060160121A1
15 GENERAL INFORMATION:
16 APPLICANT: Wyeth
17 APPLICANT: Wheth
17 APPLICANT: MUNITON: RROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
17 TILE OF INVENTION: RROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
17 FILE REPERENCE: 031896-084100 (AM 101724)
17 CURRENT APPLICATION NUMBER: US/11/348,413
17 CURRENT FILING DATE: 2005-10-05
18 PRIOR APPLICATION NUMBER: PCT/US05/035471
19 PRIOR APPLICATION NUMBER: US 11/243,445
19 PRIOR PLILING DATE: 2005-10-05
19 PRIOR FILING DATE: 2005-10-05
19 PRIOR FILING DATE: 2005-10-05
19 PRIOR FILING DATE: 2005-10-05
19 PRIOR SPELICATION NUMBER: US 60/615,573
19 PRIOR SEQ ID NOS: 1276209
10 SEQ ID NO 32920
10 LEMATH: 25
10 THE TABLE TABLE
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PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 32919
LENGTH: 25
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OTHER INFORMATION: probe
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                                                                                                                                                           TYPE: DNA ORGANISM: Artificial
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Search completed: October 16, 2006, 14:22:01 Job time : 53.2331 secs

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AX996400 Sequence CO874706 Sequence E37929 Remedy for

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Run on:

Sequence:

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Hominidae, Homo.

1 (bases 1 to 98)
Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P.,
Maggi, E. and Romagnani, S.
Molecular basis of cross-reactivity among allergen-specific human T
cells: T-cell receptor V alpha gene usage and epitope structure
Immunology 81 (1), 15-20 (1994)
                        AY390010 Heparitis
CQ149122 Sequence
CQ233796 Sequence
CQ3307710 Sequence
AND SEQUENCE
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/note="allergen-specific; mismatch(30[D->N]) when compared
with sequence im paper"
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Ното sapiens T-cell receptor alpha-chain (TcR V alpha) mRNA,
partial cds.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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GenBank staff at the National Library of Medicine created thi
entry [NCBI gibbsq 144559] from the original journal article.
Location/Qualifiers
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/gene="TCR V alpha"
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AX989552 Sequence
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
                                                nucleic search, using sw model
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1 (bases 1 to 98)
Mohapatra, S. S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P., Maggi, E. and Romagnani, S.
Molecular basis of cross-reactivity among allergen-specific human Teells: T-cell receptor V alpha gene usage and epitope structure immunology 81 (1), 15-20 (1994)
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/mol_type="mRNA"
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                  Length 98;
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                  ch 11.0%; Score 27.8; DB 5; Smilarity 57.5%; Pred, No. 1.9e+03; 50; Conservative 0; Mismatches 37;
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Pred. No. 6.2e+03;
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Homo sapiens
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Best Local Similarity 56.3
Matches 49; Conservative
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15 Invivous.
16 Tamiya,G., Makino,S., Fujimoto,K., Oka,A., Hayashi,H., Denda,A.,
16 Ininsen,S.E., Ikuta,T., Shinya,M., Endo,T., Tomizawa,M., Tokubo,E.,
16 Sato,R., Takaki,A., Nagatsuka,Y., Watanabe,H., Adachi,S.,
17 Makino,Y., Nakano,S., Yamamoto,A., Yoshida,K., Okamoto,K.,
18 Manguchi,D., Ishibashi,H., Yonekura,M., Takayama,S., Nakami,Y.,
19 Saruwateari,T., Brand,A., van Hilten,J.A., van de Watering,L.M.,
19 Direct Submission
10 Liphart,M.J., Bahram,S., Kulski,Y.J. and Inoko,H.
10 Direct Submission
11 Submitteed (12-DEC-2003) Hidetoshi Inoko, Tokai University School of
12 Submitteed (12-DEC-2003) Hidetoshi Inoko, Tokai University School of
14 Submitteed (12-Dayan (E-mail:hinoko@is.icc.u-tokai.ac.jp,
16 Medicine, Department of Genetic Information, Bohseidai, Isehara,
17 Ranagawa, 255-1193, Japan (E-mail:hinoko@is.icc.u-tokai.ac.jp,
16 Polymorphisms were confirmed by comparing with the pooled DNA
17 typing data of 88 Dutch population or 100 Australian. When there
18 was no significant difference between the Japanese and these
                                                                                                                                                                                                                                                                                                                                                                   Tamiya,G., Shinya,M., Imanishi,T., Ikuta,T., Makino,S., Okamoto,K., Furugaki,K., Matsumoto,T., Mano,S., Ando,S., Nozaki,Y., Yukawa,W., Nakashige,K., Yanaguchi,D., Ishibashi,H., Yonekura,M., Nakami,Y., Takayama,S., Endo,T., Saruwatari,T., Yagura,M., Yoshikawa,Y., Fujimoto,K., Oka,A., Chiku,S., Linsen,S.E., Giphart,M.J., Shishikawa,Y., Shizhiki,J.K., Fukazawa,T., Hashimoto,H., Kimura,M., Hoshina,Y., Shiozawa,S., Taniguchi,A., Yamanaki,T., Komai,K., Hotta,T., Mochida,J., Minezaki,T., Komai,K., Bahram,S. and Inoko,H.

Mhole genome association study of rheumatoid arthritis using 27 039 microsatellites
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/PCR conditions="denaturation 96degC 5 min, 57degC 1 min, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 72degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 sec, 57degC 1 min; 40 cycles 96degC 45 sec, 57degC 45 se
                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/note="pooled DNA of 100 Japanese unrelated individuals
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/note="sequence tagged site D10S0812i"
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|mol_type="genomic DNA"
|db_xref="taxon:9606"
|chromosome="10"
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complement(89. .109)
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Homo Bapiens (human)
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PAT 18-DEC-2003
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Genes differentially expressed in human prostate cancer and their
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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156 CAGCTCGCAGTCGGCCAGGGAGGCGGGGAGAGACGAGCGGCTCTGGCCCC 207
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0
                                 Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 16064 06-SEP-2000;
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9.8%; Score 24.8; DB 2;
Best Local Similarity 67.3%; Pred. No. 1.7e+04;
Matches 35; Conservative 0; Mismatches 17;
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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Sequence 3158 from Patent WO0160860.

    .92
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AUTHORS
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JOURNAL
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1 (bases 1 to 92)

Madards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 11980 02-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
JP 2001269182-A/11980
02-007-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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Pred. No. 1.7e+04;
0; Mismatches 17; Indels
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Edwards,J.-B.D.M., Duclert,A. and Giordano,J.-Y.
Expressed sequence tags and encoded human proteins
Patent: US 6783961-A 16064 31-AUG-2004;
FRX;
                                                                              linear
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                                                                        92 bp DNA Sequence tag and encoded human protein.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="unknown"
                                                                                                                                                      BD035734.1 GI:22577476
JP 2001269182-A/11980.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 67.3%;
Matches 35; Conservative
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PC C12P2
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Li.X.
Method, array and kit for detecting activated transcription factors
by hybridization array
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                                                                                                                                                                                                                                                                            9 cocrimentecreseseachoseccrimatercieseccascascineces
       filsue type="herpetic skin lesion"
<1. .>13
/codon start=1
/product="T cell receptor beta chain"
/protein id="AAV26660.1"
/db_xref="GI:54111803"
/translation="NVNALLGDSALYLCASSSGTPYGYTFGSGTRLTVVEDL"
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Han, K., Kim, D. and Kim, H.-J.
Vector-based method for visualizing secondary structure of RNA
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                                                                                                                                                                    Length 119;
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                                                                                                                                                                                                        41; Indels
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                                                                                                                                                                    9.7%; Score 24.4; DB 5; Local Similarity 54.4%; Pred. No. 2.4e+04; les 49; Conservative 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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INHA University Foundation; Inchon-81;
KRX;
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Sequence 145 from patent US 6696256.
AR477180.1 GI:47234454
                                                                                                                                                                                                                                                                                                                   97 TGCCACGGGCTGAGTTTCCGGCTCCAGGTT 126
                                                                                                                                                                                                                                                                                                                                         1. .96
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1 from patent US 6651010.
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1 (bases 1 to 78)
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AR431314
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Homo sapiens clone RW33 T cell receptor beta chain mRNA, partial
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                                                                                     PAT 30-JAN-2004
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                             Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                  Schlegel, R., Endege, W.O. and Monahan, J.E. Genes differentially expressed in human prostate cancer and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

1 (bases 1 to 119)

Barcy, S., Huang, M.L., Corey, L. and Koelle, D.M.

Longitudinal Analysis of Herpes Simplex Virus-Specific CD4+ Cell

Clonotypes in Infected Tissues and Blood

J. Infect. Dis. 191 (12), 2012-2021 (2005)
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                                                                                       linear
                                                                                                                                                                                                                                                                                                                                    Patent: WO 0160860-A 12327 23-AUG-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                 Sequence 12327 from Patent WO0160860.
                                                                                                                                                                                                                                                                                                                                                                                           1. .104
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="RW33"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 Crcrrccrrccracccc 80
62 CTCTTCCTTCGCTAACGCC 80
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AY751306.1 GI:54111802
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1. .78
/organism="unknown"
/mol_type="genomic DNA"
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BD034735/c
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AR734996/c
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                                                                                                                                                                                          78 AGCTICAGGICAGAGGICAGAGCIAGCTICAGGICAGAGGICAGAGGCIAGCITCAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method and kit for isolating DNA probes that bind to activated transcription factors
Patent: US 6924113-A 145 02-AUG-2005;
Panomics, Inc.; Redwood City, CA
Location/Qualifiers
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                                                                                                               Query Match 9.4%; Score 23.8; DB 2; Length 78; Best Local Similarity 59.7%; Pred. No. 3.5e+04; Matches 40; Conservative 0; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,X.
Method for screening for drug cannium transcription factor activity
Patent: US 6821737-A, 145 23-NOV-2004;
Panomics, Inc.; Redwood City, CA
Patent: US 6696256-A 145 24-FEB-2004;
Pandmics, Inc.; Redwood City, CA
Location/Qualifiers
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Sequence 145 from patent US 6821737.
AR606935.1 GI:56659110
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/mol_type="genomic DNA"
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AUTHORS
TITLE
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                             FEATURES
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                                                                                                 109 AGTITICCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
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                                                                                                                          18 AGCTTCAGGTCAGAGGTCAGAGGCTAGCTTCAGGTCAGAGGGTCAGAGAGCTACAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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JP 2001269182-A/10981
24-PEB-2000
JP 200118773
26-PEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, BIMERIC DUCLAIR, JEAN YVES
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Query Match 9.4%; Score 23.8; DB 2; Length 78; Best Local Similarity 59.7%; Pred. No. 3.5e+04; Matches 40; Conservative 0; Mismatches 27; Indels
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1 (bases 1 to 72)

Edwards, J. B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein

Patent: JP 2001269182-A 10981 02-OCT-2001;

GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Sequence tag and encoded human protein.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Unclassified.

REFERENCE 1 (bases 1 to 72)

AUTHORS Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.

AUTHORS Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.

TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: US 6783961-A 15065 31-AUG-2004;

Genset S.A.;

Location/Qualifiers

1. .72

REATURES

1. .72

Augusty Match

Query Match

9.4%; Score 23.6; DB 2; Length 72;

Best Local Similarity 69.6%; Pred. No. 4e+04;

Matches 32; Conservative 0; Mismatches 14; Indels 0;

Matches 32; Conservative 0; Mismatches 14; Indels 0;

ON 128 GCGTGTCGCCCTGAGGTTTGAGGCCCCAGACAGCCCCAGACAGCCCCAG 13

58 GCGTGGCGCCCCGGGGATCGAGCACCAGACAGACAGCAGCAGCAG 13
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Search completed: October 16, 2006, 13:38:02 Job time : 1373 secs

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Gaps

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Vовв H,
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Abv03167 Human pro
Abv12336 Human pro
Abr17318 Transcrip
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Aah68919 Human sec
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Acd76587 E. coli K
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Aak4587 Human bon
Aak18659 Human bra
Abs44245 Human liv
Abs18824 Human gen
Ach88031 Human gen
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                                                                                                             1 gggttatctgcaactgagag.....tctctcctttcgccacctcc
5.1.9
Biocceleration Ltd.
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GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                   nucleic search, using sw model
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ABV03167
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占	27-MAR-2003	(fire	(first entry)	<u> </u>		

Murine, T cell receptor; TCR; hdm2; T cell response; alpha TCR; beta TCR; antigen-recognising sequence; ARS; fusion construct; cytostatic; apoptotic; tumour; leukaemia; immunisation; ds. Polylinker Scal-Li-(Bsgl-Scal) DNA

01-MAR-2001; 2001DE-01009854

01-MAR-2001; 2001DE-01009854

(STAN/) STANISLAWSKI

Stanislawski

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New polypeptide of a murine alpha/beta T-cell receptor, useful for treating tumors and leukemia, induces specific lysis or apotosis of cells expressing hdm2 protein.

Example 2; Fig 6; 52pp; German.

This invention describes a novel murine alphabeta T-cell receptor (TCR) that mediates a hdm2 protein-specific T cell response, a fusion protein (FP) that includes the TCR and nucleic acid encoding it, alpha or betachains of a TCR that include the antigen-recognizing sequence (ARS) of an

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expression and secretion vectors
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antibody specific for aa 81-88 of hdm2 (or its complex with HLA-A2-specific antibody) and a method for identifying hdm2-specific antigens. The TCR of the invention has cytostatic and apoptotic activity. The products of the invention are useful for treatment, prevention and diagnosis of hmd2-associated diseases, particularly tumours and leukaemia, including use for passive or active immunisation. They can also be used to screen for therapeutic agents. This sequence enocodes the polylinker Scal-Li-(Bsgl-Scal) fragment used in the construction of the fusion constructs described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                       106 CTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                       Score 25.6; DB 6; Length 115; Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                         49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 TCGGGCAGGGAGGGCGGGGAGACGAGCGGCTCTGGCCCCTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 115 BP; 19 A; 33 C; 47 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5' EST, SEQ ID NO: 16064.
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                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 GGAGGGCGGGGGAGAGACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                     Gaps
                                                                                                                                                                                                    156 CAGCTCGCAGTCGGGCAGGGCGGGGGGGAGAGAGGGGGGCTCTGGCCCC 207
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                                                                  Length 92;
                                                           Query Match 9.8%; Score 24.8; DB 3; Length 9 Best Local Similarity 67.3%; Pred. No. 2.1e+03; Matches 35; Conservative 0; Mismatches 17; Indels
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Sequence 92 BP; 19 A; 24 C; 44 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate expression marker cDNA 3158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ВЪ
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25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV03167 standard; cDNA; 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-2001
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Human; colon cancer; colon cancer antigen; diagnosis; detection;

colorectal carcinoma; ss.

WO200122920-A2 Homo sapiens.

Human colon cancer antigen encoding cDNA SEQ ID NO:3242.

(first entry)

03-SEP-2001

AAH36160;

62 CTCTTCCTTCGCTAACGCC 80

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AAH36160 standard; cDNA; 105

AAH36160

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer. (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (d) assessing the prostate cell carcinogenic potential of a compound; (g)
                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patis; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
Sequence 104 BP; 9 A; 39 C; 30 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 12327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monahan JE;
                                                                                                            234 CTCTCCTTTCGCCACCTCC 252
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                                                                                                                                                                                                                                                                                                                                                               ABV12336 standard; cDNA; 104 BP
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09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-029007P.
13-DEC-2000; 2000US-0255281P.
                                                                                                                                                                               62 crcrrccrrccraccc
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2000US-0189862P.
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16-MAR-2000;
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ABV12336

ID ABV12336

XX ABV1

XX ABV1

XX Huma

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cancer-associated nucleic acid molecules (N) and proteins (P), where the cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to expression curve the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P carcinoms and cancers. AAH31709 to AH37204 and AAB77789 represent according according and anothers. AH317104 to AH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at the color of the present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 ccecnáceccecaéenaccesrcesaanreccesrceacecacecnrirensecaaa 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 CTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 24.2; DB 4; Length 105; 53.7%; Pred. No. 3.2e+03; ive 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 105 BP; 24 A; 36 C; 32 G; 8 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 5034-5035; 9803pp; English..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 CAGCTCGCAGTCGGGCAGGGAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                          Birse CE,
                                                                                                                                                                                                                                                                                                      28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                                                                                                                                                                                            99US-0157137P.
                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAG76755.
                                                                                                                                                                                                                                                                                                                                            29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                              03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM,
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84 CATGGCGGGCCAGGACGGGGGG 105

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61

174 GGAGGGGGGGGAGAGACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT 233

9.8%; Score 24.6; DB 5; Length 104; 57.0%; Pred. No. 2.5e+03;

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Indels

34;

0; Mismatches

57.0%;

45; Conservative

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Best Local Similarity

Query Match Matches 234 CTCTCCTTTCGCCACCTCC 252

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Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
AAH68919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises a method for identifying complexes between a transcription factor and another protein. The invention also comprises a method for isolating DNA probes which bind to activated transcription factors. The methods of the invention are useful for identifying transcription factor-protein interactions. The methods of the invention are also useful for facilitating the screening and identification of new drugs, characterising their mechanism of action and screening for adverse side effects based on drug's impact expression. The present DNA sequence represents a probe used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                Identifying transcription factor-protein complexes, by isolating transcription factor complexes from sample based on a specific type of factor, and identifying different proteins present in isolated complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AGTTTCCGGCTCCAGGTTCGCGTGTCGCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 AGCTICAGGICAGAGGICAGAGCIAGCTICAGGICAGAGGCCAGAGAGCTAGCTICAG 19
                                                                                     Transcription factor-related array hybridisation probe - SEQ ID No 145
                                                                                                          Probe; 88; transcription factor-protein complex; transcription factor; drug screening; drug identification; array hybridisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%; Score 23.8; DB 8; Length 78; 59.7%; Pred. No. 3.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 78 BP; 15 A; 27 C; 15 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 15065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                    ABT17318 standard; DNA; 78 BP.
                                                                                                                                                                                                                               08-JUN-2001; 2001US-00877243.
08-JUN-2001; 2001US-00877403.
08-JUN-2001; 2001US-00877705.
08-JUN-2001; 2001US-008477738.
05-SEP-2001; 2001US-00947274.
                                                                                                                                                                                                           30-MAY-2002; 2002WO-US017408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC10990 standard; cDNA; 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                (first entry)
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Matches 40; Conservative
                                                                                                                                                                                                                                                                                                   (PANO-) PANOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 GGCAGGG 175
                                                                                                                                                                                                                                                                                                                                             WPI; 2003-148829/14.
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                                                                                                                                                                  WO2002101351-A2
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                                                                10-APR-2003
                                                                                                                                             Unidentified
                                                                                                                                                                                        19-DEC-2002
                                           ABT17318;
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ID AAC10
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 15065; 71pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cervical cancer marker nucleic acid 193.
                                                                                                                                                                                                                                                                                                                                                     21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0122487P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1999;
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                                                                                                                                                                                                  EP1033401-A2
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Claim 3; Page 168; 2004pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACD76587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACD76587
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                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                isolated nucleic acid for diagnosing and treating cervical cancer and assessing and detecting compounds for treating the cancer.
                                                                                                                                                                                                                                                                                                                                                                                                      189 GACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGTCTCTCTTTCGCCAC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochip containing probes complementary with open reading frames in
Escherichia coli K12, useful for detecting gene expression and expression
                                                                                                                                                                                                                          cervical cancer with cytostatic activity. The nucleic acids and encoded by polypotrides are useful: to assess if a patient is affiliated with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                              invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGAGGTACGCGGGGGGCTGNAGTAGGCTTCGTCTTCGGNTTTTCTCTTCCTTCGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochip; gene expression; gut; diagnostic; detection; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                    9.4%; Score 23.6; DB 4; Length 97; 59.4%; Pred. No. 4.8e+03; Ive 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                              Sequence 97 BP; 7 A; 34 C; 30 G; 23 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. coli K12 MG1655 biochip probe SEQ ID 1015.
                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weber J;
                                                                                                                                                 New isolated nucleic acid for diagnosing
                                                                                                                                                                                    Claim 1; Page 137; 1051pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huber A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACD69745 standard; DNA; 100 BP.
21-DEC-1999; 99US-0171350P.
14-MAR-2000; 2000US-0189315P.
12-MAX-2000; 2000US-023791P.
09-JUN-2000; 2000US-0210600P.
21-JUL-2000; 2000US-0220114P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2001; 2001EP-00112179
                                                                                                                                                                                                                                                                                                                                                               59.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2001; 2001EP-00112179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                               38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drescher B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MWGB-) MWG-BIOTECH AG
                                                                                                 Deeds J,
                                                                                                                          WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-241155/24
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1260592-A1
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                                                                                                 Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Donner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                 containing many identical probes. The probes are nucleotide species of a containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or complementary to, a segment of an open reading frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the biochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reactivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD81540 represent oligonucleotide probes used with the biochip described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochip containing probes complementary with open reading frames in
Escherichia coli K12, useful for detecting gene expression and expression
                                                                                                                                                                                                                                                                                                                           other E. coll strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 CACGGGCTGAGTTTCCGGCTCCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 CAAGTICTGCGCCGCCTGCACCATTCGCCAGTGCCGCGCGGGTITCTGGCCAGCC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
This invention describes a novel biochip comprising probe spots,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochip, gene expression; gut; diagnostic; detection; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 100 BP; 21 A; 29 C; 38 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 8;
Pred. No. 5.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli K12 MG1655 biochip probe SEQ ID 7863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weber J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 1228; 2004pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huber A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2001; 2001EP-00112179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001; 2001EP-00112179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.3%;
Best Local Similarity 63.2%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACD76587 standard; DNA; 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MWGB-) MWG-BIOTECH AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the invention
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complementary to, a segment of an open reading frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, exectivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD8550 represent oligonucleotide probes used with the biochip described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the invention
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Sequence 100 BP; 13 A; 35 C; 29 G; 23 T; 0 U; 0 Other;

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                                                                     100 CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
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                                        Gaps
                                    0,
Score 23.4; DB 8; Length 100;
Pred. No. 5.5e+03;
0; Mismatches 21; Indels C
   9.3%;
                                      36; Conservative
                        Local Similarity
      Query Match
                                        Matches
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Oligonucleotide DmetER, SEQ ID 9. ВЪ. ADR28210 standard; DNA; 100 (first entry) 04-NOV-2004 ADR28210; RESULT 11

2-amino-4-alkylthio-butyric acid; methionine synthase; cystathionine-gamma-synthase; acylhomoserine sulfhydrylase; ss.

Synthetic

FR2851255-A1. 20-AUG-2004. 14-MAY-2003; 2003FR-00005768

18-FEB-2003; 2003FR-00001924

(META-) METABOLIC EXPLORER

Gonzales

Chateau M,

B, Soucaille PNP;

WPI; 2004-618123/60.

acid, useful for preparing L-methionine, from simple carbon source and mercaptan or its salt, have modified methionine synthase activity. strains of microorganisms that produce 2-amino-4-alkylthio-butyric

Example 1; SEQ ID NO 9; 68pp; French.

The present invention relates to a novel strain (A) of a microorganism which produces a 2-amino-4-alkylthio-butyric acid (I) by metabolising a simple sugar and a thiol (II), or its salt, and has at least one gene encoding an enzyme with modified methionine synthase (MS) activity. (A) are specifically used for fermentative production of L-methionine, which synthesis of L-Met is independent of synthesis of cysteine; the methyl mercaptan used is a toxic waste product from the petrochemical industry and synthesis of L-Met occurs in a single step from O-(acetyl or

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succinyl)-L-homoserine. The enzyme with modified MS activity is either cystathionine-gamma-synthase or an acylhomoserine sulfhydrylase, and is modified so that the substrate is reacted with (II) rather than with L-cysteine, to result in preferential conversion of the substrate to (I) or homocysteine. The present sequence was used in an example from the
                                                                                                                                                                                                                                                                                                                                       100 caccecercacriticescrecacricecerciescercreascrireageccasac 156
                                                                                                                                                                                                                                                                                                                                                                                       CAAGTTCTGCGCCGCCTGCACCATGTTCGCCAGTGCCGCGCGGTTTCTGGCCAGCC 68
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                  ch 9.3%; Score 23.4; DB 13; Length 100; 1 Similarity 63.2%; Pred. No. 5.5e+03; 36; Conservative 0; Mismatches 21; Indels 0.
                                                                                                                                                                                       Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                             invention.
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                            Matches
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ss; microorganism evolution; metabolic pathway; metabolite; biotransformation; NADPH-dependent enzyme; nucleic acid metabolism; Nucleic acid DmetER to generate evolved microorganisms. (first entry) 02-DEC-2004

ВР

ADR99734 standard; DNA; 100

RESULT 12 ADR9973 ADR99734;

lipid metabolism; sugar metabolism.

WO2004076659-A2.

10-SEP-2004.

17-FEB-2004; 2004WO-FR000354. 18-FEB-2003; 2003FR-00001924. 14-MAY-2003; 2003FR-00005768. 14-MAY-2003; 2003FR-00005769.

(META-) METABOLIC EXPLORER

06-NOV-2003; 2003FR-00013054

Zink O; Soucaille PNP, Chateau M, Gonzalez B, Meynial-Salles I,

WPI; 2004-653418/63

New evolved microorganisms with altered metabolic pathways, useful e.g for production of amino acids, are selected as mutants able to grow on defined media.

Disclosure; SEQ ID NO 1; 113pp; French.

The invention relates to a method for preparing evolved microorganisms

(A) with modified metabolic pathways comprising: (a) genetic modification

(C) a microorganism to inhibit production or consumption of a metabolite

(C) a microorganism to inhibit production or consumption of a metabolite

(C) a grown on a defined medium, thus affecting its ability to grow;

(C) growing the modified organism in the defined medium so that evolution;

(C) a cocur, optionally with addition of a co-substrate to allow evolution;

(C) a selecting as (A) cells able to grow on the medium, optionally in

(C) proteins (I) expressed by them, are useful in biotransformation

(C) processes, especially those involving NADPH-dependent enzymes,

(D) particularly synthesis of amino acids (Net, Cys, Thr, Lys or Ile) but

(D) also synthesis of mucleic acids or lipids, and metabolism of sugars.

(A) provide more efficient production of selected metabolites than parent

(C) strains. This sequence represents a nucleic acid molecule used in the

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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO: 19144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO 19144; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US000668
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                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                             WO200157276-A2
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                         06-NOV-2001
                                                                                                                                                                                                                                                                                                                                             09-AUG-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-2001
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                            AAK44587;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain; nerve degeneration; nootropic; neuroprotective; antiporvulsant; antiporvulsant; antiporvulsant; antiporvulsant; antiporvulsant; antiporvulsant; antiporvulsant; antiporvulsant; antiporvuls disease; Huntington; a disease; Parkinson; a disease; muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New protein isolated from human embryonic brain useful for treating nerv
degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (I) which has nootropic, neuroprotective, anticonvulsant, antiparty control and antidiabelic activity. (I) is useful for treating nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's disease, muscular hypoplastic lateral sclerosis, Huntington's disease, brain infarction, diabetic neuropathy and traumatic nerve degeneration. AAZ89256-289234 represent PCR primers used in the isolation and amplification of the human brain protein described in the method of the
                                                                                                                                            100 CACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCAGAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel human embryonic brain derived protein
                                                                                                                                                                                                 68
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                DB 13; Length 100;
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                                                                                                21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horie M, Hirano H, Kyushiki H, Mitsumoto Y, Mori A,
Sequence 100 BP; 15 A; 36 C; 25 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59 BP; 9 A; 23 C; 14 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.2; DB 3;
Pred. No. 5.5e+03;
0; Mismatches 18;
                                             Score 23.4; DB 13
Pred. No. 5.5e+03;
0; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human embryonic brain protein PCR primer #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 62; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                      BP.
                                           9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2%;
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                                                                                                                                                                                                                                                                                                                    AAZ89260 standard; DNA; 59
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                              36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 65.4
nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-205568/18
                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200007614-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-1999;
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                                                                                                                                                                                            12
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                                                Query Match
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                                                                                              Matches
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XX AC AAZ8
XX AC AAZ8
XX AC AAZ8
XX Huma
XX Huma
XX Homo
XX WO20
XX C C A AZ8
CC AAZ8
CC AAZ
                                                                                                                                                                                                                                                                   RESULT 13
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samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, brain expressed exon, gene expression analysis, probe, microarray, Alzheimer's disease, multiple sclerosis, schizophrenia; epilepsy, cancer,
                                                                                                                                                                                                                       86
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                                                                                                                                                                                                                       27 GTTAAGGCGTCCCCAAGTTGGAAGGCGCTTTGCTTCTGTTTTCTGGATGCAGATCCTC
                                                                                                                                                                             0; Gaps
                                                                                                                              / Match 9.2%; Score 23.2; DB 4; Length 101; Local Similarity 61.7%; Pred. No. 6.38+03; nes 37; Conservative 0; Mismatches 23; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe SEQ ID NO: 18650.
                                                                                         Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          AAK18659 standard; DNA; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157275-A2
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ઠે 셤 AAK44587 standard; DNA; 101 BP

RESULT 14 AAK44587/C ID AAK44

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 18650; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.2%; Score 23.2; DB 4; Length 101;
Best Local Similarity 61.7%; Pred. No. 6.3e+03;
Matches 37; Conservative 0; Mismatches 23; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101 BP; 36 A; 22 C; 23 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                   04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053256.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                   30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                        WPI; 2001-483446/52
09-AUG-2001
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Search completed: October 16, 2006, 13:14:41 Job time : 257 secs

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Gaps ö

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia; Butheria; Busrchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 100)

S Dum, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, 
                    AZ769498
1M0570K16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0570K16 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: K column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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Seg primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 100.
Location/Qualifiers
CN071764
CW117487
DU188381
                                                                       BZ585533
CK005996
CL952595
CD029354
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BJ965328
BJ965717
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BJ967675
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CO018108
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     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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  Mus musculus
   \begin{array}{c} \mathbf{v} \ \mathbf{o} \ \mathbf{v} \ \mathbf{o} \ \mathbf{v} \ \mathbf{o} \ \mathbf{v} \ \mathbf
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DEFINITION
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KEYWORDS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
AZ769498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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  0 0 0
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CC255380 CGVCP92TH
AW800261 MR2-UM006
DV900899 POSM06050
AZ697609 RPCT-23-2
BZ718505 60259562
BZ836170 CH240_225
AL182961 TETEXGOON
CE219192 vaa04011.
BZ987003 PUDDG92TD
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CG574657 OST207730
CG535738 OST122945
CK014560 33148Esic
CL952591 OSIKUN001
AV841732 AV841732
                                                                                                                                                                     ; Search time 2284 Seconds (without alignments) 6169.734 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                      1 gggttatctgcaactgagag......tctctcctttcgccacctcc 252
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                            GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1484138
                                                                                                                                                                                                                                                                                                                                                                                                                                              48236798 segs, 27959665780 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       nucleic search, using sw model
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CK014560
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AV841732
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DV900899
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                   US-10-604-726A-8797
252
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 120
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GSS 16-FEB-2001

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organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" |db_xref="taxon:10090" |c1one="UUGC1M0570K16" |sex="Male"

source

DV552589 2E12.dat DN773586 E1235 [C1 3F724320 bx03e03.y

CNS02660 CB219192 3B219192 BZ987003 BF724320 DV552589 DN773586

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Score

Result

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Eutheria; Barchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus. Sciurognathi; Muroidea; Murinae; Mus. Sciurognathi; Muroidea; Murinae; Mus. Sciurognathi; Musinae; Mus. Sciurognathi; Mus. BeltrandelRio,H., Ramirez-Solis,R., Richter,L.J., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jainch,R.A., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorsti., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sanda,A.T.
Whil kinase deficiency lowers blood pressure in mice a gene-trap screen to identify potential targets for therapeutic intervention processure and Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS CK014560 110 bp mRNA linear EST 04-FEB-2005 DEFINITION 33148rsicef_6492.yl Oryza sativa cv. PA648 panicle sterile cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           CG535738 82 bp mRNA linear GSS 01-OCT-2003 OST122945 Mus musculus 1295v/Ev Mus musculus cDNA clone OST122945,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 TGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGCTGAGTTTCCGGCTCCAG 123
                                                                                                                                                                                                                                                              39 CCAAGTIGGAAGGGCGCTTTGCTTTTTCTGGATGCAGAGTCCTCTGACTCCCTC 96
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                                                                                                 Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 26.2; DB 12; Length 82; 56.6%; Pred. No. 1.9e+04; ive 0; Mismatches 33; Indels
                                                                                                                                                            IndelB
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/clone_lib="Mus musculus 129Sv/Ev"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                              Score 27.6; DB 12;
Pred. No. 8e+03;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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/clone="OST122945"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
CG535738
CG535738.1 GI:37322310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GTTCGCGTGTCGCCCT 139
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                                                                                              Query Match
Best Local Similarity 67.2%;
Matches 39; Conservative
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VERSION
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SOURCE
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CK014560/c
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                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Macazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Muscidea; Murinae; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 103)
S Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Friddle,C.J., Warken,C., Warke,W., Xu,N.,
Sparks,M.J., Van Sligtenhorst.I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnkl kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
D 14610273
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                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA
   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 29; DB 11; Length 100; 71.7%; Pred. No. 3.3e+03; tive 0; Mismatches 15; Indels
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/clone="OST207730"
/cell_type="embryonic stem cell"
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/strain="129Sv/Ev"
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CG574657.1 GI:37364994
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Gaps

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TITLE

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tissue type="whole animal"
                                                                                                                                                                                                                        Email: chenchen@genomics.org.cn
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                                                                                                                                                                                                                                             Rice genomic sequence.
Class: exon-trapped.
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Matches 37; Conserv
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                                                                                                                                Oryza sativa (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wiridiplantae; Streptophyta; Bebrelata; Poaceae; BEP clade; Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 110)
1 (bases 1 to 110)
1 (bases 1 to 110)
1 (bases 1, clin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yan, J., Geng, J., Li, G., Shi, J., Liu, J., Lio, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wang, X., Mang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhang, X., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, Ji, Ji, Ji, Chen, P.,
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (indica cultivar-group)"
/mol type="mRNA"
/cultivar="PA648"
/cultivar="PA648"
/tissue_type="panicle"
/cell type="sterile"
/dev_fiage="heading/flowering"
/clome_lib="Oryza sativa cv. PA64s panicle sterile cDNA
library"
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Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
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The Genomes of Oryza sativa: A History of Duplications PLoS Biol. 3 (2), e38 (2005)
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Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
                                                                                                               Oryza sativa (indica cultivar-group)
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Seq primer: M13 Forward
High quality sequence stop: 110
PoLYA.No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yan Zhou
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CL952591/c
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1 (basea I to 99)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 CGCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAGGGCAGGGCGGGGA 186
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An analygis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bloinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80488676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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1. 110
/organism="Oryza sativa (indica cultivar-group)"
/organism="Oryza sativa (indica cultivar-group)"
/db locate="caxon 39946"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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'clone_lib="Nori Satoh unpublished cDNA library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.2%; Score 25.8; DB 13; Length 110; 1 Similarity 60.9%; Pred. No. 2.5e+04; 42; Conservative 0; Mismatches 27; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sákyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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rel: +55-11-2704922
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nes 46; Conserv
                                                                                                                                                                                               TIGR
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AW800261/c
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ORGANISM
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JOURNAL
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Matches
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VERSION
KEYWORDS
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COMMENT
                                                                    REFERENCE
                                                                                     AUTHORS
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                                                                                                    103 bp DNA linear GSS 05-OCT-2005
1098474026684 CHORI-243 Ovis aries genomic clone CH243-202P18,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OGVCP92TH ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0505P16, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Blood"
/clone_lib="CHORL-243"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
The CHORL-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 TGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAG 123
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                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                     Cocket, N.
Cocket, N.
Cother BAC End Sequences from Library CHORI-243

Unpublished (2004)

Cother GSSs: 1098474028028

Contact: Ewen Kirkness

Contact: Ewen Kirkness

The Institute for Genomic Research (TIGR; www.tigr.org)

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-795-7536

Email: ekirknesstigr.org

Sequences generated at the J. Craig Venter Institute Joint

Technology Center (JCVIJTC; http://www.venterinstitute.org/).

Original Trace: 1098474026684 Trace TI: gnl|ti|918952333

Insert Length: 184000 Std Error: 0.00 row: P column: 18

Seq primer: SP6

Class: BAC ends.
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 63
                      71
                    16 CTTCGTCTAAGTGGGGGTTGAATGGGGTTTCCCCACATTTGAGGGGTGACTTTGCTTC
                                                                                                                                                                                                                                                                                                                                        Oddy, H.
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                                                                                                                                                                                                                                                                                                 Pecora; Bovidae; Caprinae; Ovis.
1 (bases 1 to 103)
Kirkness,E., Shetty,J., de Jong,P., McEwan,J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="Texel breed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. 103
/organism="Ovis aries"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9940"
/clone="CH243-202P18"
                                                                                                                                                                                             DU408432.1 GI:77138562
GSS.
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                                                                                                                                                                                                                                    Ovis aries (sheep)
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CG255380.1 (
GSS.
Zea mays
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Matches 49; Conserv
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KEYWORDS
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CG255380/c
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DU408432
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Hominidae; Homo.

1 (bases 1 to 103)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Garcia Correa, R., Zago, M.A., Bordin, S., Costa, F.F., Garlina, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 117)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Consortium for Maize Genomics
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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/mol type="genomic DNA"
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/db xef="taxon:4577"
/clone="ZMMBMa0505P16"
/clone="Vector: pRCSK-; Site 1: HincII; 0.7-1.5 ]
methylation filtered genomic DNA library"
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llarity 57.5%; Pred. No. 2.9e+04;
Conservative 0; Mismatches 34; Indels 0;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 10737800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850, USA
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Class: methylation filtered.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWB00261.1 GI:7852131
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Gaps

; 0

33

GSS 24-JAN-2001

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/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
FCORI; Site 2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhadokigy.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Library availability, please contact fee Jong

Regiong@mail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 240 row: H column: 23

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 108)
Akao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-240H23.TJ
                                                                                                                                                                                                                                         128 GCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAGGGAGGCGGGGGAG 187
    /lab_host="DH10B"
/clone_lb="porcine skeletal muscle cDNA library (PoSM)"
/note="Organ: hind limbs; Vector: pSPORT1; Site_1: NotI;
Site_2: Sall:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPCI-23-240H23.TV RPCI-23 Wus musculus genomic clone RPCI-23-240H23, genomic survey sequence.
                                                                                                                                             Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Fax: 301 838 0200
                                                                                                                                             9.9%; Score 25; DB 10;
56.8%; Pred. No. 4.2e+04;
iive 0; Mismatches 35
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/clone="RPCI-23-240H23"
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Matches 46; Conserv
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=MK2-UM0060-170 400-203-e06&t3=2000-04-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence start: 9
High quality sequence stop: 80.
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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/dev stage="45 d and 90 d of gestation, birth, 7 wk and 1
yr of age"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 GGCCAGACAGCTCGCAGTCGGGCAGGGAGGGCGGGGAGAGACGAGGGGGCTCTGGCCCCT 208
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10.0%; Score 25.2; DB 7; Length 103;
Best Local Similarity 55.8%; Pred. No. 3.7e+04;
Matches 48; Conservative 0; Mismatches 38; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Ernst CW
Animal Science Molecular Genetics Lab
Michigan State University
B220 Anthony Hall, East Lansing, MI 48824, USA
Tel: 517 352 1941
Fax: 517 353 1699
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                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 TAATIGIACTICGGGCTCGTATTGTC 234
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/db_xref="taxon:9823"
/sex="male and female"
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CNS02660
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                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.

Is I (bases 1 to 89)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Preparation: Michael J. Brownstein (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 19.

Location/Qualifiers
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                                                                                                                                                                                BG718505 89 bp mRNA linear EST 08-MAY-2001
602696562F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828574 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                    Gaps
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                                    ö
                                                                  59 GCTTCTGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCT 107
                                                                                     GCTTTCCTTTACTCTGCGCAGAGGCCTCAGGCTCCTTCTCACGCGGGCT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 9.8%; Score 24.8; DB 2; Length 89; 1 Similarity 57.9%; Pred. No. 4.78+04; 44; Conservative 0; Mismatches 32: Indele
   DB 11; Length 108;
                                15; Indels
 Score.25; DB 11;
Pred. No. 4.2e+04;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="IMAGE:4828574"
/lab_host="DH10B"
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ch 9.9%;
1 Similarity 69.4%;
34; Conservative (
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Matches 44; Conserva
   Query Match
Best Local Similarity
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RESULT 13 BZ836170

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (Dases 1 to 116)

RS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvattsbeyn,A., Gebregeorgia,B., Chen,D., Riggs,F., de Jong,P., Crawford,A.M. and McEwan,J.C.

Bovine BAC End Sequences from Library CHORI-240

AL Umpublished (2003)

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Email: szhao@tigr.org

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/Dacpac/bordar/Doinformail. This work was undartaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.

Plate: 225 row: C column: 14

Seq primer: Sp6

Class: BAC ends.
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BZB36170 116 bp DNA linear GSS 18-MAR-2003
CH240_225C14.TJ CHORI-240 Bos taurus genomic clone CH240_225C14,
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ALJ82961.1 GI:7821065
ALJ82961.1 GI:7821065
GSS; genence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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63.3%; Pred. No. 4.9e+04;
tive 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="breed: Hereford"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9913"
/clone="CH240_225C14"
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                                                      genomic survey sequence.
                                                                                     BZ836170
BZ836170.1 GI:29063528
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                                                                                                                                                                        Bos taurus (cattle)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : Submitted (12-APR-2000) Genoscope - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)
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                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
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Virgin,S., Tianxiang,S., Karst,S., Wobus,C., Lay,M., Clifton,S., Pape,D., Marxa,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Teagareishvili,R., Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
                                      , Bouneau, L., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                      Roest Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fish
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="240C22"
/clone_lib="G"
/note="Genoscope sequence ID : COAG240BB11SP1
end : PUC-Ori"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
Petradontoidea; Tetraodontidae; Tetraodon.
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Contact: Skip Virgin
RNA Expression in Diseased Tissues by RDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA Expression in Diseased Tissues by RDA
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Pred. No. 4.9e+04;
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Best Local Similarity 52.0%;
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COMMENT
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REFERENCE
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                    REFERENCE
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Adaptington University School of Medicine

4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
741: 314 286 1800

Fmail: set@watson.wustl.edu

Email: set@watson.wustl.edu

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Email: set@watson.wustl.edu

Email: set@watson.wustl.edu

Email: set@watson.wustl.edu

Size is 300bp. The insert also has same adaptor sequence on both end. The sequence of the adaptor is: 5'-ATACGTGCAGGTGGTTACATCTG

Seq primer: -40UP from Glabco.

And Evpe="Mark" Homo sapiens"

And Lype="Mark" Homo sapiens"

And Lorate Type="Mark" Homo sapiens"

And Lorate Type="Mark" Homo sapiens"

And Home insert also has same adaptor size is

300bp. The insert also has same adaptor sequence on both end in the sequence of the adaptor is:

S'-ARACGTGGAGGTGGTRACATCTG -3'"

Query Match

9.8%; Score 24.6; DB 4; Length 107;

Best Local Similarity 95.2%; Pred. No. 5.5e+04;

Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

And Interpretation of the mark of the sequence of the adaptor correct of the adaptor is:

S-ARACGTGGAGGTGGAGGTGGAGGTCTTGGTCTGGCAGGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGA
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15277, A
113, Appl
11, Appl
2027, Appl
57, Appl
57, Appl
57, Appl
57, Appl
4514, Ap
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Sequence 1, Appli
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                                                              October 16, 2006, 13:41:14 ; Search time 124 Seconds (without alignments) 3802.576 Million cell updates/sec
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Biocceleration Ltd.
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US-09-877-78C-145

US-09-513-999C-15065

US-09-513-999C-23785

US-09-513-999C-23785

US-09-513-999C-23785

US-09-513-999C-22785

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US-09-662-133A-13

US-09-662-57

US-09-162-64-674D-57

US-09-165-616-57

US-09-165-616-57

US-09-513-999C-29691

US-09-513-999C-29691

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                                                                                                                                                                 1403666 segs, 935554401 residues
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Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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        GenCore (c) 1993
                                                                                                 US-10-604-726A-8797
252
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seg length: 120
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Match
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Perfect score:
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; sequence 16064, Application US/09513999C
; sequence 16064, Application US/09513999C
; patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dunds Milne Edwards, J.B.
; APPLICANT: Dunclert, A.
; APPLICANT: Dunclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PILE NEFERRING: 59.US2.REG
; CURRENT FILING DATE: 2000-02-24
; FILE REFERRING DATE: 1999-02-26
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16064
; LENGTH: 92

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                                                                                                                                                                           27, Appl
13592, A
16, Appl
20, Appl
7790, Ap
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2971, Ap
90, Appl
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S-QUENCE 1, Application US/09210305C
Patent No. 6651010
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A vector-based method for
TITLE OF INVENTION: A vector-based method for
                                                            2856, Ap
2856, Ap
1, Appli
18431, A
8314, Ap
5830, Ap
3264, Ap
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                                        US-08-905-223-68
US-10-131-827-2856
US-08-362-454-1
US-08-621-976-18431
US-09-621-976-18431
US-09-621-976-18431
US-09-925-540-5830
US-09-422-978-3264
US-09-9422-978-3264
US-09-634-368-16
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US-09-634-368-90
US-08-134-3468-90
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Pred. No. 3.6e+02;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BACHMAN & LAPOINTE, P.C.
STREET: Suite 1201, 900 Chapel Street
CITY: New Haven
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                          US-09-789-529-6
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Best Local Similarity 67.3%;
Matches 35; Conservative
TYPE: DNA
CORGANISM: Homo sapiens
US-09-513-999C-16064
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US-09-877-143A-145/c
1S-09-877-43A-145/c
; Sequence 145, Application US/09877243A
; Patent No. 6696256
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-702
; CURRENT APPLICATION NUMBER: US/09/877,243A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GCCGCCUGCAAAUUGCGCUGUGCUCCUGUGCUACGGCCUGUGGCUGGACUGCCU 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 GCCGTCCCCAAGTTGGAAGGGCGCTTTGCTTCTGTTTTCTGGATGCAGAGTCCTCTGACT 91
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COUNTRY: U.S.A.
ZIP: 06510-2802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.6%; Score 24.2; DB 3;
Best Local Similarity 43.5%; Pred. No. 5.6e+02;
Matches 30; Conservative 11; Mismatches 28;
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                                                                        COMPUTER: IBM
COMPUTER: IBM
COMPUTER: IBM
CORRENT SYSTEM: WINDOWS 95/98
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,305C
FILING DATE: 11-Dec-1998
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23.8; DB 3
Pred. No. 7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Hybridization probe MP74 US-09-877-243A-145
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-877-705A-145/c
Sequence 145, Application US/09877705A
Patent No. 6821737
GENERAL INFORMATION:
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nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 CCCTCTGCC 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Li, Jason

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TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
TITLE OF INVENTION: FACTOR ACTIVITY
FILE REFERENCE: 26757-704
CURRENT APPLICATION NUMBER: US/09/877,705A
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 162
SOFTWARE PATENTIAL VERSION 3.1
SEQ ID NO 145
LENGTH: 78
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APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: TRANSCRIPTION FACTORS
FILE REFERENCE: 26757-701
CURRENT APPLICATION NUMBER: US/09/877,738C
CURRENT PAILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin version 3.1
SEQ ID NO 145
LENGTH: 78
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US-09-513-999C-15065/c
Sequence 15065, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
APPLICANT: FITHE REPERENCE: 59.US2.REG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 23.8; DB 3; Length 7 59.7%; Pred. No. 7e+02; ive 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Hybridization probe MP74
US-09-877-705A-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Hybridization probe MP74
US-09-877-738C-145
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; Sequence 145, Application US/09877738C
; Patent No. 6924113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 59.73
Matches 40; Conservative
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62 CTGTGCCCCACAGCCACCGCCTTCTTTCCAGATCCAGGGTCTCCAGGAGCTC 10

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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AGONICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT PILING DATE: 2001-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 15685
LENGTH: 66
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                                                                                                                                                                                                                                                                                                                                                         9.4%; Score 23.6; DB 3; Length 72; 69.6%; Pred. No. 7.8e+02; tive 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 GCGTGTCGCCCTGAGGTTTGAGGCCAGACAGCTCGCAGTCGGGCAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GCGTGGGGCCCCGGGGGATCGAGGCCATCCAGCACAGAGGCGGCCAG 13
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SSEQ ID NO 15065
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-866-108A-15685/c
; Sequence 15685, Application US/09866108A
; Patent No. 6686188
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HANZEL, David K.
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Best Local Similarity 69.03
Thes 32; Conservative
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
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US-09-866-108A-15685
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APPLICANT:
APPLICANT:
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US-09-513-999C-23785

Sequence 23785, Application US/09513999C

Patence 23785, Application US/09513999C

Patence 23785, Application US/09513999C

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 678361

FILE REPERBNCE: 59.US2.REG

CURRENT PILING DATE: 200-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PAtent.pm

SEQ ID NO 23785

LENGTH: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FACELIANT: Duclett, A. APPLICANT: Giordano, J.Y. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59.US2.REG CURRENT FILEMERRACE: 59.US2.REG CURRENT FILEMERRACE: 59.US2.REG CURRENT FILING DATE: 2000-02-24 PRIOR PPLICATION NUMBER: US 60/122,487 PRIOR PPLING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOUTHARE: Patent.pm SEQ ID NOS: 36681 SEQ ID NO 15277
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Pred. No. 2.1e+03;
0; Mismatches 41; Indels
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8.8%; Score 22.2; DB 3; Length 6
Best Local Similarity 64.7%; Pred. No. 2.1e+03;
Matches 33; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 CGGGCTGAGTTTCCGGCTCCAGGTTCGC 129
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; Sequence 15277, Application US/09513999C
; Patent No. 6783961
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Best Local Similarity 53.4%;
Matches 47; Conservative (
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; ORGANISM: Homo sapiens
US-09-513-999C-15277
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ORGANISM: Homo sapiens
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US-09-347-613C-13/c
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86 CIGACICCCICITGCCACGGCIGAGITICCGGCICCAGGITCGCGIGTCGCCC 138

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-662-183A-13
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US-09-513-999C-20278
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; ORGANISM: Homo sapiens
US-09-367-927A-1
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APPLICANT: Johansen, Teit E.
APPLICANT: Johansen, Teit E.
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Halesn, Claus
TITLE GF INVENTION: No. 6734284el Neurotrophic Factors
TITLE REFERENCE: 19313-001 DIV
CURRENT APPLICATION NUMBER: US09/662,183A
CURRENT APPLICATION NUMBER: US09/662,183A
CURRENT APPLICATION NUMBER: US09/662,183A
CURRENT APPLICATION NUMBER: US09/662,183A
PRIOR APPLICATION NUMBER: US09/662,183A
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR PLICATION NUMBER: USN 60/097,774
PRIOR APPLICATION NUMBER: USN 60/097,774
PRIOR PLING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-13
                                                                           APPLICANT: JOHANSATION:
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Blom, Nikolaj
APPLICANT: Hansen, Claus
TITLE OF INVENTION: No. 659313361 Neurotrophic Factors
FILE REFERENCE: NeuroSearch 19313-001
CURRENT APPLICATION NUMBER: US/09/347,613C
CURRENT APPLICATION NUMBER: US/09/347,613C
CURRENT APPLICATION NUMBER: US/09/347,613C
CURRENT APPLICATION NUMBER: DANISH 1998 00904
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR PRILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-10-05
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.8%; Score 22.2; DB 3;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23;
Sequence 13, Application US/09347613C
Patent No. 6593133
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09662183A Patent No. 6734284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-662-183A-13/c
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LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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ITLEO FO INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 20278
LENGTH: 115
                                                                                                                            0; Gaps
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8.8%; Score 22.2; DB 3; Length 115;
Best Local Similarity 61.0%; Pred. No. 2.4e+03;
Matches 36; Conservative 0; Mismatches 23; Indels
            Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09367927A

Batent No. 6300126

GENERAL INFORMATION:
APPLICANT: GRUMMT, INGRID
APPLICANT: RAINWEG, MITTLERER
APPLICANT: RAINWEG, MITTLERER
APPLICANT: APPLICANT: RAINWEG, MITTLERER
TITLE OF INVENTION: EXPRESSION VECTOR FOR THE PERMANENT
TITLE OF INVENTION: EXPRESSION OF FOREIGN DNA
FILE REFERENCE: 1929043US00
CURRENT APPLICATION NUMBER: US/09/367,927A
CURRENT FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 1999-10-20
SOFTWARE: FastSEQ for Windows Version 3.0
Query Match 8.8%; Score 22.2; DB 3; Length 1 Best Local Similarity 61.0%; Pred. No. 2.4e+03; Matches 36; Conservative 0; Mismatches 23; Indels
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US-09-513-999C-20278/c
; Sequence 20278, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumag Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.7
Matches 33; Conservative
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Search completed: October 16, 2006, 13:43:27
Job time : 125 secs
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63 GGGTGGGGGCGCCCCGGGAGAGACAGCACCTCGCAGCCCCAGAATTTGTTTTCGCTTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/964,624D
FILING DATE: 21-OCTUBER-1992
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 10-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: BARRY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 33,215
REFERENCE/DOCKET NUMBER: MEXOS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-442-062-57/c
US-08-442-062-57/c
; Sequence 57, Application US/08442062
; Patent No. 5595877
; GENERAL INFORMATION:
APPLICANT: GOLD, LARRY M.
APPLICANT: TUBEK, CRAIG
; TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
; TITLE OF INVENTION: ACIDS ON THE BASIS OF
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GOLD, LARRY M.
APPLICANT: TUERK, CRAIG
TITLE OF INVENTION: METHOD OF SELECTING NUCLEIC
TITLE OF INVENTION: ACIDS ON THE BASIS OF
TITLE OF INVENTION: STRUCTURE
NUMBER OF SEQUENCES: 83
CORRESSONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 B. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
                                                                              RESULT 14
US-07-964-624D-57/c
; Sequence 57, Application US/07964624D
; Patent No. 5496938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 TTTGAGGCCAGAC 156
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STRANDEDNESS: single
TOPOLOGY: linear
US-07-964-624D-57
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84 CTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGG 143
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TITLE OF INVENTION: STRUCTURE
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
SADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STRIE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/5 inch, 1.44 MB
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
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FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
CLASSIFICATION: 435
BRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
RIDRA APPLICATION NUMBER: 07/714,131
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: BATAY J. SWANBON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXO5/D1
TELEPHONE: (303) 793-3333
TELEPHONE: (303) 793-3433
INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: INCHARACTERISTICS:
LENGTH: 86 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,062
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US-10-310-914A-16611/c
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; ORGANISM: Human
US-10-310-914A-16611
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1: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO7_PUBCONB.seq:*

2: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO8_PUBCONB.seq:*

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4: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO9_PUBCONB.seq:*

5: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO9_PUBCONB.seq:*

6: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO9_PUBCONB.seq:*

7: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO0_PUBCONB.seq:*

8: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO0_PUBCONB.seq:*

9: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO0_PUBCONB.seq:*

10: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO0_PUBCONB.seq:*

11: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO0_PUBCONB.seq:*

12: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USO0_PUBCONB.seq:*

13: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USOO_PUBCONB.seq:*

14: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USOO_PUBCONB.seq:*

15: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USOO_PUBCONB.seq:*

16: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USOO_PUBCONB.seq:*

16: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USOO_PUBCONB.seq:*

16: /EMC_Celerra_SIDS3/ptodate/2/pubpna/USOO_PUBCONB.seq:*
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Sequence 16551, A
Sequence 3158, Ap
Sequence 3227, Ap
Sequence 17067, A
Sequence 145, App
Sequence 6323, Ap
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                                                                                                                         ; Search time 814 Seconds (without alignments) 3804.035 Million cell updates/sec
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               GenCore version 5.1.9
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6 US-11-173-902-22
US-10-67-124A-16551
US-10-357-930-3158
US-10-357-930-12327
US-10-106-698-1252
US-10-1106-698-1252
US-09-877-705A-145
US-09-877-705A-145
US-09-877-738A-145
US-09-877-493A-145
US-09-877-499-115
US-10-795-595-145
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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seq length: 120
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Sequence 16611, Application US/10310914A

Publication No. US20060003322A1

Publication No. US2006000332A1

REBREAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Boinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICANION WHOBER: US/10/310,914A

CURRENT PILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SEQ ID NO 16611

LENGTH: 67
                                              Sequence 192, App
Sequence 16455, A
Sequence 15685, A
Sequence 13685, A
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 1425, App
Sequence 1425, App
Sequence 1425, App
Sequence 9222, App
Sequence 9222, App
Sequence 9222, App
Sequence 9222, App
Sequence 12025, App
Sequence 20316, Appl
Sequence 20316, Appl
Sequence 20316, Appl
Sequence 234, Appl
Sequence 234, Appl
Sequence 234, Appl
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                          US-10-029-186-21234

US-09-908-975-792

US-09-908-975-792

US-09-908-975-792

US-09-928-6108-15685

US-10-425-115-142012

US-10-661-984A-13

US-10-661-984A-13

US-10-661-984A-13

US-10-806-793-13

US-10-806-793-13

US-10-806-793-13

US-10-910-914A-265

US-10-918-95-222

US-10-918-95-222

US-10-918-914A-2035

US-10-918-914A-2035

US-10-918-914A-2035

US-10-918-95-37

US-10-918-95-37

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Publication No. US20060057611A1
GENERAL INFORMATION:
APPLICANT: KAO, H. PIN
APPLICANT: LAO, KAI QIN
APPLICANT: JONES, ROBERT
TITLE OF INVENTION: LOG-LINEAR AMPLIFICATION
FILE REFERENCE: 375461-021US
CURRENT APPLICATION NUMBER: US/11/173,902
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| APPLICANT: Schlegel, Wilson
| APPLICANT: Schlegel, Wilson
| APPLICANT: Endege, Wilson
| APPLICANT: Endege, Wilson
| APPLICANT: Endege, Wilson
| APPLICANT: Endege, Wilson
| APPLICANT: Monahan, John
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
| TITLE OF INVENTION: HUMAN PROSTATE CANCER
| TITLE OF INVENTION: HUMAN PROSTATE CANCER
| TITLE OF INVENTION: HUMBER: 09/185,276
| CURRENT APPLICATION NUMBER: 06/183,319
| PRIOR APPLICATION NUMBER: 60/189,862
| PRIOR APPLICATION NUMBER: 60/189,862
| PRIOR PRIOR PRIOR ENDER: 2000-02-17
| PRIOR PELING DATE: 2000-06-25
| PRIOR PELING DATE: 2000-06-18
| PRIOR FILING DATE: 2000-06-18
| PRIOR PELING DATE: 2000-06-18
| PRIOR PELING DATE: 2000-07-18
| PRIOR PELING DATE: 2000-07-18
| PRIOR PILING DATE: 2000-07-18
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Publication No. USZO040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monshan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MAI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-02-16
42 CTGAGTTTTCAGGCAGGCAGGCAGGCAGGCAGGCAGGTAGGAGTACAGCAC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 deracecededeagacecededecededecedecedecederageserricerricegrifri 61
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9.8%; Score 24.6; DB 9; Length 103;
Best Local Similarity 57.0%; Pred. No. 1.2e+03;
Matches 45; Conservative 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                             Sequence 3158, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                        198 CT 199
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US-10-357-930-3158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 TCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16551, Application US/10674124A
; Publication No. US20040197797A1
; GENERAL INFORMATION:
APPLICANT: INONGO, Hidetoshi
APPLICANT: TAMIYA, Gen
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
CURRENT APPLICATION NUMBER: US/10/674,124A
CURRENT FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR FILING DATE: 2000-04-13
; PRIOR FILING DATE: 2002-09-28
; PRIOR FILING DATE: 2002-09-28
; PRIOR FILING DATE: 2002-09-28
; PRIOR SPLICATION NUMBER: JP2002-3327516
; PRIOR SPLICATION NUMBER: JP2002-332869
; RIOR APPLICATION NUMBER: JP2002-09-28
; RUMBER OF SEQ ID NOS: 27110
; LEMCTH: 109
                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; US-11-173-902-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 7.8e+02;
0; Mismatches 28; Indels
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CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION WUMBER: 60/584,665
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.3
SEQ ID NO 22
LENGTH: 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0%;
Matches 42; Conservative
                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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Sequence 145, Application US/08877705A

Sequence 145, Application US/08877705A

Publication No. US20030008283A1

GENERAL INFORMATION:

APPLICANT: Li, Jason

TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT

TITLE OF INVENTION: PACTOR ACTIVITY

FILE REFERENCE: 26757-704

CURRENT PAPLICANTION NUMBER: US/09/877,705A

CURRENT PILING DATE: 2001-08-16

NUMBER OF SEQ ID NOS: 162

SOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 145

LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                 Sequence 17067, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A

NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 17067
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                                                                                                                                                            83
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                                                                                                              96 CTGCCACGGGCTGAGTTTCCGGCTCCAGGTTCGCGTGTCGCCCTGAGGTTTGAGGCCCAGA
                                                                                                                                                         24 ccécnaceccecadenacedercegaanrecegeregaeceaegenrirengeeaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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               Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.5%; Score 24; DB 11; Length 93; Best Local Similarity 51.8%; Pred. No. 1.9e+03; Matches 29; Conservative 7; Mismatches 20; Indels
                                                             Indels
          Query Match
9.6%; Score 24.2; DB 6;
Best Local Similarity 53.7%; Pred. No. 1.6e+03;
Matches 44; Conservative 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%; Score 23.8; DB 3; Best Local Similarity 59.7%; Pred. No. 2.1e+03; Matches 40; Conservative 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Hybridization probe MP74
                                                                                                                                                                                                          156 CAGCTCGCAGTCGGGCAGGGAG 177
                                                                                                                                                                                                                                                             84 CATGGCGGGCAGGACGGGGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-310-914A-17067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-877-705A-145
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Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: 2002-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 GGAGGGGGGGGAGAGACGACGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24.6; DB 9;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%; Scor.
57.0%; Pred. No. 1.1.
0; Mismatches
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR PELING DATE: 2000-02-17
PRIOR PELING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-1-18
PRIOR PILING DATE: 2000-1-18
PRIOR PILING DATE: 2000-1-13
PRIOR PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 0502-03-27
PRIOR APPLICATION NUMBER: DCT/USO0/26524
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1909-09-29
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFUMARE: PATENTIN VET. 3.0
SEQ ID NO 3252
LENGTH: 105
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LOCATION: (28)...(28)
OTHER INFORMATION: n equals a,t,g, o:
NAME/KEY: misc_feature
LOCATION: (40)...(40)
OTHER INFORMATION: n equals a,t,g, o:
NAME/KEY: misc_feature
LOCATION: (53)...(53)
OTHER INFORMATION: n equals a,t,g, o:
NAME/KEY: misc_feature
LOCATION: (72)...(72)
OTHER INFORMATION: n equals a,t,g, o:
NAME/KEY: misc_feature
LOCATION: (77)...(77)
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US-10-106-698-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 CTCTCCTTTCGCCACCTCC 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 57.0
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-357-930-12327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-10-106-698-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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GENERAL INFORMATION:
ADDITION:
APPLICANT: Li, Jason
TITLE OF INVENTION: METHOD FOR IDENTIFYING A DISEASE STATE BASED ON A DETECTED MIXTURE
TITLE OF INVENTION: ACTIVATED TRANSCRIPTION FACTORS
FILE REFERENCE: 26757-703
CURRENT APPLICATION NUMBER: US/09/877,403A
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin version 3.1
SEQ ID NO 145
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Li, Xianqiang
TITLE OF INVENTION: METHOD, ARRAY AND KIT FOR DETECTING ACTIVATED TRANSCRIPTION FACTOF
FILE REPERBENCE: 267577-702.301
CURRENT APPLICATION NUMBER: US/10/779,595
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 09/877,243
PRIOR PELLING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 162
SOFTWARE PATENTIN VERSION 3.1
SEQ ID NO 145
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23.8; DB 4; Length 78;
Pred. No. 2.1e+03;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.4%; Score 23.8; DB 8; Length 78; Best Local Similarity 59.7%; Pred. No. 2.1e+03; Matches 40; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Hybridization probe MP74
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                                                                                                                                            RESULT 11
2.09-877-403A-145/c
; Sequence 145, Application US/09877403A
; Publication No. US20040214166A1
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; Sequence 145, Application US/10779595
; Publication No. US20040132090A1
; GENERAL INFORMATION:
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Best Local Similarity 59.7%;
Matches 40; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
169 GGCAGGG 175
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                                                        18 GTCAGAG 12
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                                                                                                                                                                                              GENERAL INFORMATION NO. USECUSION 199741

APPLICANT: Li, Xianqiang
TITLE OF INVENTION: METHOD FOR DETECTING TRANSCRIPTION FACTOR-PROTEIN INTERACTIONS
FILE REPRENCE: 26757-705
CURRENT APPLICATION NUMBER: US/09/947,274
CURRENT APPLICATION NUMBER: US/09/947,274
FRIOR APPLICATION NUMBER: US/09/977,738
PRIOR FILING DATE: 2000-06-08
PRIOR PELING DATE: 2000-06-08
PRIOR PELING DATE: 2000-06-08
PRIOR PELING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: US/09/877,403
PRIOR PILING DATE: 2000-06-08
PRIOR PILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: US/09/877,705
PRIOR PILING DATE: 2000-06-08
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Publication No. US20030022173A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
TITLE OF INVENTION: TRANSCRIPTION FACTORS
FILLE REPRENCE: 255757-01
CURRENT APPLICATION NUMBER: US/09/877,738A
CURRENT PILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 162
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 145
LENGTH: 78
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59.7%; Pred. No. 2.1e+03;
iive 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 78;
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US-09-947-274-145
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                                                                                                                                               ; Sequence 145, Application US/09947274
; Publication No. US20030017499A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial sequence
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   18 GTCAGAG 12
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Matches 40; Conserv
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US-09-877-738A-145/c
                                                                                                                      -09-947-274-145/c
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APPLICANT: Algales, Paul A.
APPLICANT: Algales, Paul A.
APPLICANT: Algales, Paul A.
APPLICANT: Algales, Paul A.
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Corisa Corporation
TITLE OF INVENTION: Composations and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Composations and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352003-01
CURRENT FILING DATE: 2001-11.06
PRIOR FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: US 60/190, 479
PRIOR FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: US 60/200, 709
PRIOR PELICATION NUMBER: US 60/200, 779
PRIOR APPLICATION NUMBER: US 60/200, 799
PRIOR APPLICATION NUMBER: US 60/200, 999
PRIOR APPLICATION NUMBER: US 60/201, 999
PRIOR APPLICATION NUMBER: US 60/220, 904
PRIOR PILING DATE: 2000-05-20
PRIOR PILING DATE: 2000-05-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000
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60.0%; Pred. No. 3e+03;
tive 0; Mismatches 26; Indels
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 6323
LENGTH: 120
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Publication No. US20030078396A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-796-692-6323
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US-10-040-862-6323
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS OF STATEMENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/190, 479
PRIOR APPLICATION NUMBER: 60/200, 545
PRIOR APPLICATION NUMBER: 60/200, 545
PRIOR APPLICATION NUMBER: 60/200, 303
PRIOR FILING DATE: 2000-04-29
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200, 999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/22, 903
PRIOR PRILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/22, 903
PRIOR PRILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/22, 903
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; Sequence 6323, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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COTHER INFORMATION: DmetER
US-10-781-499-1
                                                                                    RESULT 13
US-10-781-499-1
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Query Match 9.3%; Score 23.4; DB 6; Length 120;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 39; Conservative 0; Mismatches 26; Indels 0; Gaps
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Search completed: October 16, 2006, 13:57:18 Job time : 815 secs

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Sequence 258, App
Sequence 82, Appl
Sequence 3264, Ap
Sequence 424752,
Sequence 2971, Ap
Sequence 90, Appl
Sequence 90, Appl
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198, App
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47, Appl
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419451,
890, Appl
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US-11-365-566-82
US-11-376-566-82
US-11-266-748A-424752
US-11-266-748A-307408
US-11-266-748A-307408
US-11-266-748A-300647
US-11-266-748A-300647
US-11-194-055-199
US-11-194-055-199
US-11-194-055-199
US-11-191-244-63
US-11-369-140-46
US-11-369-140-47
US-11-369-140-47
US-11-368-413-10828
US-11-266-748A-419451
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US-11-365-556-83
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Maximum Match 100%
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υι	25	19.2	7.6	107	œ r	US-11-266	US-11-266-748A-411535 US-11-244-330A-6708	Sequence		
טט	27	19		61		US-11-296	-931-1	Sequence		
υ	28	19	7	118		US-11-314	US-11-314-834-4644	Sequence	4644, Ap	
	59	18.8	7	114		US-11-043	1-842-279	Sequence		
	90	18.6	7	66		US-11-217	-529-173876	Sequence	173876,	
	15	9.6	- [907		US-11-266	-748A-420020	Sequence	232793	
U	9 K	18.4		47		US-11-370	1-584-612	Sequence	612,	
	34	18.4	7	51		US-11-143	1-642-1090	Sequence	1090, Ap	
	35	18.4	7	75		US-11-348	3-413-1748	Sequence	1748	
	36	18.4		77		US-10-834	1-268-4016	Sequence	4016	
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•	4 0	18.4	7	113		US-11-348	1-413-9862	Sequence	9862, Ap	
	41	18.2	7	20		US-10-554-711-648	1-711-648	Sequence		
	42	18.2	7	20	9	US-10-554	1-759-648	Seguence		
O	43	18.2	7	9	8	US-11-069-910-4	9-910-46	Sequence	46,	
ţ	4 4 4 7	180		96 -	9 1	US-10-531	1-545-10 0-072-15	Seguence	10, App1	
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						ALIGNMENTS	IENTS			
RES US-	RESULT 1 US-11-04	RESULT 1 US-11-043-824-258/c	.258/c							
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	TITLE	o de	VENTION:	THERE	Š Š	TITLE OF INVENTION: NOVEL NUCLECTIVE AND AMINO TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF C	THEREOF FOR DIAGNOSIS OF CARDIAC DISEASE		and Sineson of	
٠	FILE	REFERE NT ADD	SNCE: 184	7.1007 NIMBER	:	8/11/043.8	124			
	CURRE	NT FIL	ING DATE	2005	-01	CURRENT FILING DATE: 2005-01-27				
O.	NUMBE.	NUMBER OF SE	SEQ ID NO.	S: 452						
	LENG	LENGTH: 102	25							
	TYPE	TYPE: DNA ORGANISM:	TYPE: DNA ORGANISM: Artificial	a.						
	FEAT	FEATURE:		1			4			
, us-	11-04	OTHER INFORMA S-11-043-824-258	UTHEK INFORMATION: SYNCHECIC 1-043-824-258	Synche	112	orranincreorrae	ופסכזמפ			
Ome	Nuery Sest L Latche	Match ocal S s 46	Query Match Best Local Similarity Matches 46; Conser	vat	8.7%; 53.5%; ive	Sco Pre 0;	DB 7; Ler 3.8e+03; thes 40;	ngth 102; Indels 0;	Gaps 0;	
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q		26	GTCCGAGA	CACTITIC	_F.					
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	ENERA	L INFC	RMATION:			ı				

APPLICANT: LADNER, ROBERT C.
APPLICANT: COREN, EDWARD H.
APPLICANT: COREN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROCKEY, KRISTIN L.
APPLICANT: HOET, RENE
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
TITLE OF INVENTION: DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS

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Sequence 3264, Application US/11370584

Publication No. US20060177863A1

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chem. Daniel
TITLE OF INVENTION: Biallalic markers for use in constructing a high
TITLE OF INVENTION: Biallalic markers for use in constructing a high
TITLE OF INVENTION: Biallalic markers for use in constructing a high
TITLE OF INVENTION: Biallalic markers
FILE REFERENCE: GENSET.020CP1
CURRENT FILING DATE: 2006-03-08

PRIOR PILING DATE: 2008-03-08

PRIOR FILING DATE: 1999-10-20

PRIOR PELICATION NUMBER: US 09/298,850

PRIOR PELICATION NUMBER: US 09/298,850

PRIOR PLING DATE: 1999-10-20

PRIOR PELING DATE: 1999-10-21

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1998-11-23

PRIOR FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 3264
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FILE REFERENCE: DYAX/002
CURRENT APPLICATION NUMBER: US/11/365,556
CURRENT FILING DATE: 2006-02-28
FURIOR APPLICATION NUMBER: US/09/837,306
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 428
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
LENGTH: 98
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 35; Conserva
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### APPLICANT: Willigan, Mailingan, Mailinga
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59.3%; Pred. No. 1e+04;
tive 0; Mismatches 24; Indels
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8.2%; Score 20.6; DB 6; Length 100;
Best Local Similarity 59.3%; Pred. No. 9.8e+03;
Matches 35; Conservative 0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (1319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR PELICATION NUMBER: EP 04105483.4
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR PELING DATE: 2005-03-14
                                            PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US 08/976,288
PRIOR PILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/129,930
PRIOR PILING DATE: 1993-09-30
PRIOR FILING DATE: 1992-11-12
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PATCHIN VETSION 3.3
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 300647, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnston, Patrick APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 59.34
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Primer US-10-874-990B-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-300647
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US-11-266-748A-300647/c
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Sequence 90, Application US/10874990B
Sequence 90, Application US/10874990B
Sequence 90, Splication OS US20060216303A1
Septence 90, Application No. US20060216303A1
GENERAL INFORMATION:
APPLICANT: SOMANTA LIMITED
APPLICANT: CERIANT, Roberto L.
APPLICANT: PETERSON, Jerry A.
APPLICANT: PADLAN, Eduardo A.
TITLE OF INVENTION: FROCESSES AND PRODUCTS WITH MODIFIED ANTIBODIES OF HUMAN MILK FAT TITLE OF INVENTION: GLOBULE SPECIFICITY
FILE REFERENCE: SOMA1140-4
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                                                                                                                                                                                                                                  59 GCTTCTGTTTTCTGGATGCAGAGTCCTCTGACTCCCTCTGCCACGGGCTGAGTTTCCGGC 118
                                                                                                                                                                                                                                                                                    15 GCTTGACTGTACAGCATGTTGTTTCCTATCGCTCCTGGCGTCAGGGCTTCATGTTCCGGT 74
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                                                                                                                  Length 106;
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                                                                                                               Query Match 8.3%; Score 20.8; DB 8; Length 10
Best Local Similarity 55.6%; Pred. No. 8.7e+03;
Matches 40; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 24
; OTHER INFORMATION: 99-21310-416 : polymorphic base A or G
US-11-370-584-2971
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8.2%; Score 20.6; DB 7;
Best Local Similarity 70.3%; Pred. No. 7.7e+03;
Matches 26; Conservative 1; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                         119 TCCAGGTTCGCG 130
                                                                                                                                                                                                                                                                                                                                                                                                    75 GACTGATTACCG 86
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-307408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
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HEREALL LIVENCHALLOW:

APPLICANT: Carlo M.

APPLICANT: Liu, Chang-Gong

APPLICANT: Callin, George, A.

APPLICANT: Callin George, A.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS MITH

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS. ASSOCIATED CHROMOSOMAL.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER. ASSOCIATED CHROMOSOMAL.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER. ASSOCIATED CHROMOSOMAL.

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CALLOGE OF PRIOR PELICATION NUMBER: 60/542, 949

PRIOR FILING DATE: 2004-02-09

PRIOR PELICATION NUMBER: 60/542, 940

PRIOR PELICATION NUMBER: 60/542, 940

PRIOR PELICATION NUMBER: 60/580, 797

PRIOR PELING DATE: 2004-06-18

PRIOR PELING DATE: 2004-06-18

PRIOR PELING DATE: 2004-06-18

PRIOR PELING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 60/580, 797

PRIOR PELING DATE: 2004-06-18

NUMBER: PRETER PERSOR FOR WINDOWS VERSION 4.0

SEQUID NO 277

LENGTH: BA
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8.1%; Score 20.4; DB 8;
Best Local Similarity 61.1%; Pred. No. 1.1e+04;
Matches 33; Conservative 0; Mismatches 21;
                                         PRIOR FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: 60/580,797
PRIOR FILING DATE: 2004-06-18
NUMBER OF SEQ ID NOS: 663
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 198
LENGTH: 86
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GENERAL INFORMATION: APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 277, Application US/11194055; Publication No. US20060105360A1; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/580,959
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; ORGANISM: Homo sapiens
US-11-194-055-198
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US-11-194-055-277
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US-11-169-140-46/c
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Sequence 198, Application US/11194055

Publication No. US20060105360A1

GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
APPLICANT: Claim, George, A.
APPLICANT: Claim, George, A.
APPLICANT: Claim, George, A.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
FILE REFERENCE: 3589.1018-008

CURRENT FILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: E05-07-29

PRIOR APPLICATION NUMBER: 60/542,929

PRIOR PILING DATE: 2004-02-09

PRIOR FILING DATE: 2004-02-09
                                                                                                                                                                                                                                                                                                                          APPLICANT: Croce, Carlo M.
APPLICANT: Calin, Chang-Gong
APPLICANT: Calin, Cang-Gong
APPLICANT: Calin, Calin, George, A.
APPLICANT: Calin, Casorge, A.
APPLICANT: Calin, George, A.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER-ASSOCIATED CHROMOSOMAL
TITLE OF INVENTION: Microrna LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
TITLE OF INVENTION: PEATURES
FILE REFERENCE: 3589.1018-008
CURRENT PILLING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: G0/542,929
PRIOR PILLING DATE: 2004-02-09
PRIOR PILLING DATE: 2004-06-18
PRIOR FILLING DATE: 2004-06-18
PRIOR FILLING DATE: 2004-06-18
PRIOR FILLING DATE: 2004-06-18
PRIOR FILLING DATE: 2004-06-18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199
                                                                                                                                                                                              Sequence 199, Application US/11194055
Publication No. US20060105360A1
GENERAL INFORMATION:
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Gaps

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Length 86;

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APPLICANT: HOUSTON, Lou, L.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: HARLEY, Steephen
APPLICANT: GLANT: HARLEY, Steephen
APPLICANT: GLANT: HARLEY, Steephen
TITLE OF INVENTION: MATHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
TITLE OF INVENTION: MATHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
TITLE OF INVENTION: MATHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
TITLE OF INVENTION: MATHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
TITLE OF INVENTION: MATHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS
CURRENT APPLICATION NUMBER: US 60/248,819
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-03
PRIOR FILING PRIOR 
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US-11-191-244-64/c

Sequence 64, Application US/11191244

Publication No. US20060134103A1

Sequence 64, Application Wo. US20060134103A1

Sequence 64, Application No. US20060134103A1

APPLICANT: HAWLEY, STEPHEN B.

TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE

TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS

TITLE REPRENCE: 05-220/1301

CURRENT APPLICATION NUMBER: US/11/191,244

CURRENT FILING DATE: 2006-07-27

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 64

LENGTH: 95
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7.9%; Score 20; DB 8; Length 95;
Best Local Similarity 58.3%; Pred. No. 1.5e+04;
Matches 35; Conservative 0; Mismatches 25; Indels
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7.9%; Score 20; DB 8; Length 95;
Best Local Similarity 58.3%; Pred. No. 1.5e+04;
Matches 35; Conservative 0; Mismatches 25; Indels
                                                                                       GENERAL INFORMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
APPLICANT: HOUSTON, Lou, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: HOUSTON, Lou, L.

APPLICANT: SHERIDAN, Philip, J.

APPLICANT: HOUSTON, Philip, J.

APPLICANT: HAWLEY, Stephen

APPLICANT: HAWLEY, Stephen

APPLICANT: CHAPIN, Steven

TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE

TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE

TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE

TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE

TITLE OF INVENTION NUMBER: US 60/267,601

PRIOR PELICATION NUMBER: US 60/248,819

PRIOR APPLICATION NUMBER: US 60/248,478

PRIOR APPLICATION NUMBER: US 60/248,478

PRIOR APPLICATION NUMBER: US 60/237,929

PRIOR PELING DATE: 2000-10-02

PRIOR FILING DATE: 2001-10-02

PRIOR PELING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: 09/949,039

PRIOR PELING DATE: 2001-10-02

NUMBER OF SEQ ID NOS: 143

SEQ ID NO 46

**IBNGTH: 80
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Publication No. US20060134103A1

GENERAL INFORMATION:

APPLICANT: HAMLEY, STEPHEN B.

TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE

TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS

FILE REFRENCE: 057220/1301

CURRENT APPLICATION NUMBER: US/11/191,244

CURRENT APPLICATION NUMBER: US/11/191,244

CURRENT FILING DATE: 2005-07-27

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PATENTIN VEY: 2.1

LENGTH: 80
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. OTHER INFORMATION: Description of Artificial Sequence: Primer
US-11-191-244-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.9%; Score 20; DB 8; Length 80; Best Local Similarity 58.3%; Pred. No. 1.4e+04; Matches 35; Conservative 0; Mismatches 25; Indels
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7.9%; Score 20; DB 8; Length 80;
Best Local Similarity 58.3%; Pred. No. 1.4e+04;
Matches 35; Conservative 0; Mismatches 25; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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US-11-191-244-63/c
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US-11-169-140-47/c
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